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OM protein - protein search, using sw model

Run on: May 2, 2002, 08:48:18 ; Search time 12.56 Seconds

(Without alignments)  
576.916 Million cell updates/sec

Title: US-09-823-038a-33

Perfect score: 1779

Sequence: 1 RRAPCCSCRCRCRCGMPSHR.....VLPTGDVMSRPDGSYLNRPL 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Tsgued\_patents\_AA.\*

1: /cgn2\_6/ptodata/2/laa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/laa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/laa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/laa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/laa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/laa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1779	100.0	322	4	US-09-383-586-33
2	1371	77.1	529	4	US-09-383-586-31
3	1029	57.8	439	4	US-09-383-586-32
4	391	22.0	801	4	US-09-383-630-6
5	378	21.2	806	4	US-09-383-630-3
6	375.5	21.1	335	1	US-08-471-570-14
7	375.5	21.1	643	1	US-08-471-570-6
8	375.5	21.1	769	1	US-08-471-570-8
9	373	21.0	816	1	US-07-640-029-1
10	371.5	20.9	821	2	US-08-451-822A-13
11	364.5	20.5	820	1	US-07-921-807B-3
12	364.5	20.5	820	1	US-08-441-944A-3
13	364.5	20.5	820	1	US-08-439-992A-1
14	360.5	20.3	351	5	PCT-US93-05703-2
15	360.5	20.3	817	1	US-07-640-029-2
16	360.5	20.3	822	1	US-07-921-807B-4
17	360.5	20.3	822	1	US-08-459-236-2
18	360.5	20.3	822	1	US-08-441-944A-4
19	360.5	20.3	822	4	US-08-451-822A-12
20	360.5	20.3	822	4	US-08-439-992A-2
21	359.5	20.2	822	1	US-07-997-133-1
22	350	19.7	126	4	US-09-383-586-30
23	349.5	19.6	820	1	US-08-166-717D-6
24	308	17.3	300	1	US-07-640-029-5
25	308	17.3	300	4	US-08-439-992A-5
26	307	17.3	526	1	US-08-471-570-4
27	307	17.3	652	1	US-08-471-570-10

28	306	17.2	302	1	US-07-921-807B-7	Sequence 7, Appli
29	305	17.2	302	1	US-08-441-944A-7	Sequence 12, Appli
30	305	17.1	240	1	US-08-471-570-12	Sequence 6, Appli
31	304	17.1	302	1	US-07-640-029-6	Sequence 8, Appli
32	304	17.1	302	1	US-07-921-807B-8	Sequence 6, Appli
33	304	17.1	302	1	US-08-441-944A-8	Sequence 5, Appli
34	304	17.1	302	4	US-08-439-992A-6	Sequence 4, Appli
35	304	17.1	731	1	US-07-921-807B-5	Sequence 5, Appli
36	304	17.1	731	1	US-08-441-944A-5	Sequence 4, Appli
37	304	17.1	733	1	US-08-439-992A-3	Sequence 3, Appli
38	304	17.1	733	1	US-07-640-029-4	Sequence 6, Appli
39	304	17.1	733	1	US-07-921-807B-6	Sequence 6, Appli
40	304	17.1	733	1	US-08-441-944A-6	Sequence 4, Appli
41	304	17.1	733	4	US-08-439-992A-4	Sequence 3, Appli
42	301	16.9	729	1	US-07-640-029-3	Sequence 6, Appli
43	282.5	15.9	729	1	US-08-070-165F-6	Sequence 6, Appli
44	282.5	15.9	729	2	US-08-885-418-6	Sequence 6, Appli
45	282.5	15.9	731	1	US-08-070-165F-10	Sequence 10, Appli
46	282.5	15.9	731	2	US-08-885-418-10	Sequence 10, Appli
47	237	13.3	1651	4	US-09-540-245A-18	Sequence 18, Appli
48	234.5	13.2	1101	3	US-08-986-465-2	Sequence 2, Appli
49	233	13.1	1297	4	US-09-540-245A-17	Sequence 17, Appli
50	233	13.1	1395	4	US-09-540-245A-15	Sequence 15, Appli
51	230.5	13.0	946	5	PCT-US95-08493-13	Sequence 13, Appli
52	228	12.8	1381	4	US-09-540-245A-16	Sequence 16, Appli
53	225	12.6	615	2	US-08-752-307B-9	Sequence 9, Appli
54	210.5	11.8	1091	3	US-08-986-465-5	Sequence 5, Appli
55	208	11.7	868	1	US-08-374-834-1	Sequence 1, Appli
56	208	11.7	868	4	US-08-644-271-1	Sequence 19, Appli
57	207	11.6	434	4	US-09-540-245A-19	Sequence 19, Appli
58	207	11.6	1447	5	US-09-041-886-25	Sequence 25, Appli
59	207	11.6	1447	5	PCT-US94-05277-2	Sequence 2, Appli
60	206	11.6	478	5	PCT-US95-08493-15	Sequence 15, Appli
61	206	11.6	860	5	PCT-US95-08493-21	Sequence 21, Appli
62	206	11.6	860	5	PCT-US95-08493-21	Sequence 21, Appli
63	204	11.5	869	2	US-08-374-834-16	Sequence 16, Appli
64	204	11.5	869	2	US-08-644-271-29	Sequence 29, Appli
65	204	11.5	1501	2	US-08-447-464-3	Sequence 3, Appli
66	204	11.5	1501	2	US-08-716-679-3	Sequence 3, Appli
67	202	11.4	630	2	US-08-752-307B-14	Sequence 14, Appli
68	197.5	11.1	1018	1	US-08-408-420A-6	Sequence 6, Appli
69	197.5	11.1	1018	1	US-08-408-420A-6	Sequence 6, Appli
70	197.5	11.1	1018	3	US-08-040-741-6	Sequence 6, Appli
71	197.5	11.1	1018	3	US-08-040-741-6	Sequence 6, Appli
72	197	11.1	1911	1	US-08-348-006B-5	Sequence 5, Appli
73	197	11.1	1911	4	US-08-800-825A-5	Sequence 5, Appli
74	197	11.1	1911	4	US-09-158-657-5	Sequence 5, Appli
75	197	11.1	1911	5	PCT-US94-10166-5	Sequence 5, Appli
76	196.5	11.0	1018	1	US-08-452-052-2	Sequence 2, Appli
77	196.5	11.0	605	2	US-08-752-307B-8	Sequence 8, Appli
78	193.5	10.9	607	2	US-08-752-307B-12	Sequence 12, Appli
79	190.5	10.7	462	2	US-08-752-307B-7	Sequence 7, Appli
80	190.5	10.7	465	2	US-08-752-307B-5	Sequence 5, Appli
81	180	10.1	612	2	US-08-752-307B-11	Sequence 11, Appli
82	166.5	9.4	661	2	US-08-795-868B-14	Sequence 14, Appli
83	164	9.2	596	2	US-08-752-307B-13	Sequence 13, Appli
84	163.5	9.2	287	2	US-08-414-657D-48	Sequence 48, Appli
85	163.5	9.2	304	2	US-08-414-657D-46	Sequence 46, Appli
86	163.5	9.2	304	2	US-08-414-657D-46	Sequence 46, Appli
87	163.5	9.2	325	2	US-08-414-657D-41	Sequence 41, Appli
88	163.5	9.2	325	2	US-08-414-657D-41	Sequence 41, Appli
89	160.5	9.0	287	2	US-08-414-657D-45	Sequence 45, Appli
90	160.5	9.0	310	2	US-08-414-657D-47	Sequence 47, Appli
91	160.5	9.0	315	2	US-08-414-657D-43	Sequence 43, Appli
92	160.5	9.0	338	2	US-08-414-657D-43	Sequence 43, Appli
93	160.5	9.0	338	2	US-08-795-868B-16	Sequence 16, Appli
94	160	9.0	601	2	US-08-986-485-4	Sequence 4, Appli
95	159.5	8.9	140	3	US-09-188-930-184	Sequence 184, App
96	158.5	8.9	340	4	US-08-810-116-8	Sequence 8, Appli
97	158.5	8.9	1356	2	US-07-930-518A-8	Sequence 8, Appli
98	158.5	8.9	1356	4	US-09-098-707A-2	Sequence 2, Appli
99	157	8.8	1356	4	US-08-414-657D-60	Sequence 60, Appli
100	155.5	8.7	338	2		

## ALIGNMENTS

```
RESULT 1
US-09-383-586-33
; Sequence 33, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevlin
; APPLICANT: Kumble, Rene
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; FILE REFERENCE: 11000.1037cl
; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Human
US-09-383-586-33

Query Match          100.0%; Score 1779; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.5e-150;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRAAPCCSCRCRCMGSHRPPEAPQRRRTWMSHGRWPAHCAAVVEGDPPLTM 60
DB 1 RRAAPCCSCRCRCMGSHRPPEAPQRRRTWMSHGRWPAHCAAVVEGDPPLTM 60
QY 61 WTDGRTIHSGWRFVLPQGLKVKOVERDAGVYCKATNGFGLSVNTLVLDISP 120
DB 61 WTDGRTIHSGWRFVLPQGLKVKOVERDAGVYCKATNGFGLSVNTLVLDISP 120
QY 121 GKESLGPSSSGOEDPASQOMARPRPTOPSKMRRIARPVSSVRLKCVASGHPRPD 180
DB 121 GKESLGPSSSGOEDPASQOMARPRPTOPSKMRRIARPVSSVRLKCVASGHPRPD 180
QY 181 TWMKDDQALTRPEAAERPRKKKWTLSKLNLRPEDSGKYTCRVSNRAGAINATYKVDIORT 240
DB 181 TWMKDDQALTRPEAAERPRKKKWTLSKLNLRPEDSGKYTCRVSNRAGAINATYKVDIORT 240
QY 241 RSKPVLTGTHPVNTVDFGTTSFQCKVNSDVKPVYIOMLKRVYGAEGRNSTIDVGQK 300
DB 241 RSKPVLTGTHPVNTVDFGTTSFQCKVNSDVKPVYIOMLKRVYGAEGRNSTIDVGQK 300
QY 301 FVVLPTGDVWSRPDGSYLKPL 322
DB 301 FVVLPTGDVWSRPDGSYLKPL 322

RESULT 2
US-09-383-586-31
; Sequence 31, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevlin
; APPLICANT: Kumble, Rene
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; FILE REFERENCE: 11000.1037cl
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; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Mouse
US-09-383-586-31
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Query Match          77.1%; Score 1371; DB 4; Length 529;
Best Local Similarity 93.4%; Pred. No. 5.6e-114;
Matches 255; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
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QY 50 PVESDPEPLMTWKDGTTHSGWSRFVLPQGLKVKOVERDAGVYCKATNGFGLSVN 109
DB 48 PVESDPEPLMTWKDGTTHSGWSRFVLPQGLKVKOVERDAGVYCKATNGFGLSVN 107
QY 110 YTLIVLDDISPGKESLGPSSSGOEDPASQOMARPRPTOPSKMRRIARPVSSVRLK 169
DB 108 YTLIVLDDISPGKESLGPSSSGOEDPASQOMARPRPTOPSKMRRIARPVSSVRLK 167
QY 170 CVASGHPRPDITWKKDDQALTRPEAAERPRKKKWTLSKLNLRPEDSGKYTCRVSNRAGAIN 229
DB 168 CVASGHPRPDITWKKDDQALTRPEAAERPRKKKWTLSKLNLRPEDSGKYTCRVSNRAGAIN 227
QY 230 ATYKVDIORTSKRPVLTGTHPVNTVDFGTTSFQCKVNSDVKPVYIOMLKRVYGAEGR 289
DB 228 ATYKVDIORTSKRPVLTGTHPVNTVDFGTTSFQCKVNSDVKPVYIOMLKRVYGAEGR 287
QY 290 HNSTIDVGQKFEVVLPTGDVWSRPDGSYLKPL 322
DB 288 HNSTIDVGQKFEVVLPTGDVWSRPDGSYLKPL 320
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RESULT 3
US-09-383-586-32
; Sequence 32, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevlin
; APPLICANT: Kumble, Rene
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; FILE REFERENCE: 11000.1037cl
; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Mouse
US-09-383-586-32
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Query Match          57.8%; Score 1029; DB 4; Length 439;
Best Local Similarity 93.7%; Pred. No. 1.1e-83;
Matches 194; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
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QY 116 DDISPGKESLGPSSSGOEDPASQOMARPRPTOPSKMRRIARPVSSVRLKCVASGH 175
DB 23 DDISPGKESLGPSSSGOEDPASQOMARPRPTOPSKMRRIARPVSSVRLKCVASGH 82
QY 176 PRPDITWKKDDQALTRPEAAERPRKKKWTLSKLNLRPEDSGKYTCRVSNRAGAINATYKVD 235
DB 83 PRPDITWKKDDQALTRPEAAERPRKKKWTLSKLNLRPEDSGKYTCRVSNRAGAINATYKVD 142
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Qy 236 VIQTRSKPVLGTGHPVNTTVDFGCTTSFOCKVRSDVKPVIQMLKRVYEGAGRHNSIID 295
Db 143 VIQTRSKPVLGTGHPVNTTVDFGCTTSFOCKVRSDVKPVIQMLKRVYEGAGRHNSIID 202
Qy 296 VGGOKFVLPPTGVDVWSRPGSYLNKPL 322
Db 203 VGGOKFVLPPTGVDVWSRPGSYLNKPL 229

RESULT 4
US-09-383-630-6
; Sequence 6, Application us/09383630A
; Patent No. 6265632
GENERAL INFORMATION:
APPLICANT: Avner Yaron et al.
TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
FACTOR RECEPTOR ASSOCIATED
CHONDRODYSPLASIA
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSER: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
to an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,630A
FILING DATE: 26-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 1402/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 801
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-383-630-6

Query Match 22.0%; Score 391; DB 4; Length 801;
Best Local Similarity 32.1%; Pred. No. 1,4e-26;
Matches 102; Conservative 50; Mismatches 132; Indels 34; Gaps 9;
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Qy 173 SCHRPDITWKKDDOALF---RPEAEPRKKKTLISLNLRPEDSCKYTCRVSNRAGIN 229
Db 173 AGNPTPSISWLNKNEKFEGRHIGGILKHQOWSLWESVPSDRGNTCVVENFGSIR 232
Qy 230 ATYKVDVIQTRSKPVLGTGHPVNTTVDFGCTTSFOCKVRSDVKPVIQMLKRVYEGAGR 289
Db 233 QYTLIDVLEKSPHRIIIOAGLPANOTAILGSDVEFHCKVYSDAOPHIOMLKHEV----- 287
Qy 290 HNSTIDVGGOKFV-VLPT 306
Db 288 NGSVKGPDGTPYVTVLKT 305

RESULT 5
US-09-383-630-3
; Sequence 3, Application us/09383630A
; Patent No. 6265632
GENERAL INFORMATION:
APPLICANT: Avner Yaron et al.
TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
FACTOR RECEPTOR ASSOCIATED
CHONDRODYSPLASIA
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSER: Mark M. Friedman c/o Anthony Castorina
STREET: 2001 Jefferson Davis Highway, Suite 207
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead* Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
Windows version 3.11
SOFTWARE: Word for Windows version 2.0 converted
to an ASCII file
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,630A
FILING DATE: 26-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 1402/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-562553
TELEFAX: 972-3-562554
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 806
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-383-630-3

Query Match 21.2%; Score 378; DB 4; Length 806;
Best Local Similarity 31.8%; Pred. No. 2.1e-25;
Matches 96; Conservative 54; Mismatches 118; Indels 34; Gaps 10;
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Db 84 S-ERVLPORLOVLNASHEDSGAYSCRORLTO--RVLCFHSVRYTDAESSGDDEDED 139  
QY 129 SSSGGEDPASOOWARPRFTOPSKMRRVYIARPVGSSVRLKCVASGHPREDITWMMKDOA 188  
Db 140 EADDTGVDGTAPYW-----TRPERMDKKLLAIPAANTVTRRCRPAAGNPITSISLAKGRE 194  
QY 189 LT---RPEAAEPKKKWTLSLKLRLPDSGKYTCRVSNRAGAINATYKVDTQRTSRKPY 245  
Db 195 FRGEHRIGGJIKLRHOQSLVMSVPSDRGNNTCVENKRGSIROTYYTLDLVLESPHRPI 254  
QY 246 LTHPTVNTVDFGTTSPQCKYRSDVKPYIOWLKRYEGABEGHNSTIDVGOKFY-VL 304  
Db 255 LQGLLANQAVYAGSDVEYFCKVYSDAQPHIOWLKHEV-----NGSKVGPDTGPTVTL 309  
QY 305 PT 306  
Db 310 KT 311

RESULT 6  
US-08-471-570-14  
Sequence 14, Application US/08471570  
Patent No. 5750371  
GENERAL INFORMATION:  
APPLICANT: IGARASHI, Koichi  
APPLICANT: SEMOO, Masaharu  
APPLICANT: WATANABE, Tatsuya  
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,570  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/149,664  
FILING DATE:  
APPLICATION NUMBER: US 07/743369  
FILING DATE: 16-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: LINEK, Ernest V  
REGISTRATION NUMBER: 29822  
REFERENCE/DOCKET NUMBER: 40897  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-570-14

Query Match 21.1%; Score 375.5; DB 1; Length 355;  
Best Local Similarity 29.9%; Pred. No. 1,1e-25;  
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;

QY 23 PPEAFQRMWTRSHGWRPAGPICAANVPYEG-----DPPPLTMMTKDGRITHSQWSRF 75

Db 15 PEEPTKYQI-----SQPEYVVAAPGESLEVRCLLKDAAYISWTKDG--VHLGPNNR 64  
QY 76 RVL-PQGLAKVOYREDAGYVCATNGFSGLSYNTLVLLDIPSKESLGPDSGGQ 134  
Db 65 TVLIGELYIQTGATPPRDSGYACTASRTVSEWYFVWNTDAISSGD-----EDDTGA 120  
QY 135 EDPASQ---OWAPRFPQSKMRRVYIARPVGSSVRLKCVASGHPREDITWMMKDOALT- 190  
Db 121 EDVSESNKRRAPYWTNTKMEKRLHAIPAANTVTRRCRPAAGNPFTMRKLNKEFEKQ 180  
QY 191 --RPEAAEPKKKWTLSLKLRLPDSGKYTCRVSNRAGAINATYKVDTQRTSRKPYLTG 248  
Db 181 EHRIGGYKVRNQHMSLIMESVPSDKGNNTCVENEGSINHHTYHLDVLESPHRPI 240  
QY 249 THPTVNTVDFGTTSPQCKYRSDVKPYIOWLKRYE-----YAGN-----RHNSTIDV 296  
Db 241 GLPANNASTVVGSDVEYFCKVYSDAQPHIOWIKHVERKSGYGPDLPLYLKLHSG--T 297  
QY 297 GGOKFVVLPTGDVWSRPDGSYLNK 320  
Db 298 NSSNAEVLALFNVTEDAGEYICK 321

RESULT 7  
US-08-471-570-6  
Sequence 6, Application US/08471570  
Patent No. 5750371  
GENERAL INFORMATION:  
APPLICANT: IGARASHI, Koichi  
APPLICANT: SEMOO, Masaharu  
APPLICANT: WATANABE, Tatsuya  
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,570  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/149,664  
FILING DATE:  
APPLICATION NUMBER: US 07/743369  
FILING DATE: 16-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: LINEK, Ernest V  
REGISTRATION NUMBER: 29822  
REFERENCE/DOCKET NUMBER: 40897  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617)523-6440  
TELEX: 200291 STRE UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 643 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-570-6





TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-640-029-1

Query Match 21.0%; Score 373; DB 1; Length 816;  
Best Local Similarity 30.1%; Pred. No. 5,9e-25;

Matches 89; Conservative 46; Mismatches 115; Indels 46; Gaps 8;

QY 20 RPP-PEAPQRTKSHGMPAGPHCAAVPYEG-----DPPILTMW 61  
DB 22 RPSSTLEQAPW-----GAPVESEFLVHPGDLQRLRLDQVGSINW 66  
QY 62 TKDRTHSGWSPRVLPOGLKQYVEREDAGVYVCKATNGPGLSVNTLVLDISP 121  
DB 67 LRQVQALAE-NRTRIGEVEVDSPADSGIACVTSFSGS-DTTTSSVNDLPS 124  
QY 122 KESIGPSSSGGE-----DPASQWARRPTOPSKMRRVYIARPVGSSVRLKCVASGH 175  
DB 125 SEDDDDDSSSEKKKEKTDNTKPNVAPYWTSPKMKKLAHVPAKTKVKKCPSSGT 184  
QY 176 PRDITMKDQALTRP-----AAEPKKKWTLSKMLRPEDSGKTYCRVSNRAGAINAT 231  
DB 185 PNPLRLKNGKEF-KPDHIGYKXATWTSIIMDSVPSDKGNTYCIENEGSINH 243  
QY 232 YKVDIORTSKSVLGTGHEVNTTVDFGTTSPQCKVRSQVDPVYIOMLKRVEGAE 287  
DB 244 YQDVVERSHRPIQAGLPANTVALGNSVEFMCKYSDPHIQMLKHEMGSK 299

RESULT 10

US-08-451-822A-13  
Sequence 13, Application US/08451822A  
Patent No. 5863888

GENERAL INFORMATION:

APPLICANT: Dione, Craig A  
APPLICANT: Crumley, Greg  
APPLICANT: Jaye, Michael C  
APPLICANT: Schlessinger, Joseph  
TITLE OF INVENTION: Fibroblast Growth Factor Receptors  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Rhone-Poulenc Rorer Legal Department  
STREET: 500 Arcola Road  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,822A  
FILING DATE: 26-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/323,430  
FILING DATE: 14-OCT-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/934,372  
FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/549,587  
FILING DATE: 06-JUL-1990

ATTORNEY/AGENT INFORMATION:

NAME: Savitzky, Martin

REGISTRATION NUMBER: 29,699

REFERENCE/DOCKET NUMBER: A0496E

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 454-3816  
TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 821 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-451-822A-13

Query Match 20.9%; Score 371.5; DB 2; Length 821;  
Best Local Similarity 31.6%; Pred. No. 8.1e-25;

Matches 90; Conservative 50; Mismatches 112; Indels 33; Gaps 8;

QY 23 PPEAPQRTKSHGMPAGPHCAAVPYEG-----DPPILTMKQGRTHSGWSPR 75  
DB 35 PEEPPRTYQI-----SQPEYVAAPGSLERVLCKLMDAAVSWTKDG--VHLAPNN 84  
QY 76 RVL-POGLKQYVEREDAGVYVCKATNGPGLSVNTLVLDISPRESIGPSSSGQ 134  
DB 85 TVLIGETLQKATPRDQGLACTASRYVDSFTWYVNTDAISSGD---EDDTDA 140  
QY 135 EDPASQ---QWARRPTOPSKMRRVYIARPVGSSVRLKCVASGHPDITMKDQALT- 190  
DB 141 EDFVSESNKRAPYVNTNEMKMKRLHAVPAANTVAFRCAGAGNPMTRLKNGKEFK 200  
QY 191 --RPEAEPKKKWTLSKMLRPEDSGKTYCRVSNRAGAINATYKVDIORTSKSVLGT 248  
DB 201 EHRIGYKVNQMSLIMSVPDSKGYTCVYENEGSINH7YHIDVVERSHRPILOA 260  
QY 249 THPVNTVDFGTTSPQCKVRSQVDPVYIOMLKRVE-----YGAEG 288  
DB 261 GLPANSYVGGYVERCVKYSBQPHIQMLKHEVNGSKYGDG 305

RESULT 11

US-07-921-807B-3  
Sequence 3, Application US/07921807B  
Patent No. 5474914

GENERAL INFORMATION:

APPLICANT: SPAETE, RICHARD  
TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
TITLE OF INVENTION: OF VIRAL PROTEINS  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSER: CHIRON CORPORATION  
STREET: 4560 Horton Street - R440  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608-2916

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/921,807B  
FILING DATE: 29-SEP-1992

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MCCLUNG, BARBARA G.

REGISTRATION NUMBER: 33,113

REFERENCE/DOCKET NUMBER: 0209.001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 601-2708

TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 820 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein  
US-07-921-807B-3

Query Match 20.5%; Score 364.5; DB 1; Length 820;  
Best Local Similarity 30.4%; Pred. No. 3,4e-24;  
Matches 88; Conservative 43; Mismatches 115; Indels 43; Gaps 8;

QY 20 RPP--PEAQRWTRMSHGWRPAGPHCAAVPYEG-----DPPPLTW 61  
DB 22 RSPFTLEPQAQPM-----GAPVESEFLVHGDLLQLRCLRDVDGSI 66  
QY 62 TKDGRTHSGMSRFRVLPGGLKQVERDAGYVVCATNGFGLSVNTLVLDISPG 121  
DB 67 LRDSVQLAES-NRRRTIGEVEVDSPADSGLYACTSSPSGS-DITYFSVNSDALPS 124  
QY 122 KESLGPSSSGGQOE---DPAQOMARPRFTQPSKMRRIARVPVSSVRLKCVASGHRP 178  
DB 125 SEDDDDDSSSEKEKDNTKPNPAPYWTSPKMEKKLAHVPAKTYKFCPSGTPNP 184  
QY 179 DITMKDDQALTRPE---AAEPKKKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKV 234  
DB 185 TLRMLKNGKER-KPDHRIGGKVRATWSTIMDSVPSDKGNTYCIYENEGSINHYYQL 243  
QY 235 DVIQTRSKPYLTGTHPVNTTVDFGTTSFQCKVRSVDKPYIQLKRYE 283  
DB 244 DVERSPHRPIQLAGLPANKTVLGSNVEFMCKYSDPQPHIQLKHTE 292

## RESULT 12

US-08-441-944A-3  
; Sequence 3, Application US/08441944A  
; Patent No. 5767250  
; GENERAL INFORMATION:  
; APPLICANT: SPAETE, RICHARD  
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
; TITLE OF INVENTION: OF VIRAL PROTEINS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: 4560 Horton Street - R440  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,944A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/921,807  
; FILING DATE: 29-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MCCLUNG, BARBARA G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0209.001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2708  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 820 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-441-944A-3

Query Match 20.5%; Score 364.5; DB 1; Length 820;  
Best Local Similarity 30.4%; Pred. No. 3,4e-24;  
Matches 88; Conservative 43; Mismatches 115; Indels 43; Gaps 8;

QY 20 RPP--PEAQRWTRMSHGWRPAGPHCAAVPYEG-----DPPPLTW 61  
DB 22 RSPFTLEPQAQPM-----GAPVESEFLVHGDLLQLRCLRDVDGSI 66  
QY 62 TKDGRTHSGMSRFRVLPGGLKQVERDAGYVVCATNGFGLSVNTLVLDISPG 121  
DB 67 LRDSVQLAES-NRRRTIGEVEVDSPADSGLYACTSSPSGS-DITYFSVNSDALPS 124  
QY 122 KESLGPSSSGGQOE---DPAQOMARPRFTQPSKMRRIARVPVSSVRLKCVASGHRP 178  
DB 125 SEDDDDDSSSEKEKDNTKPNPAPYWTSPKMEKKLAHVPAKTYKFCPSGTPNP 184  
QY 179 DITMKDDQALTRPE---AAEPKKKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKV 234  
DB 185 TLRMLKNGKER-KPDHRIGGKVRATWSTIMDSVPSDKGNTYCIYENEGSINHYYQL 243  
QY 235 DVIQTRSKPYLTGTHPVNTTVDFGTTSFQCKVRSVDKPYIQLKRYE 283  
DB 244 DVERSPHRPIQLAGLPANKTVLGSNVEFMCKYSDPQPHIQLKHTE 292

## RESULT 13

US-08-439-992A-1  
; Sequence 1, Application US/08439992A  
; Patent No. 625454  
; GENERAL INFORMATION:  
; APPLICANT: Kiefer, Michael C.  
; APPLICANT: Pablo, Valenzuela D.T.  
; TITLE OF INVENTION: Expression and Use of Human Fibroblast  
; TITLE OF INVENTION: Receptor  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Chiron Corporation  
; STREET: 4560 Horton Street  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439,992A  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chung, Ling-Fong  
; REGISTRATION NUMBER: 36,482  
; REFERENCE/DOCKET NUMBER: 0165.004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 510-923-2704  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 820 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-439-992A-1

Query Match 20.5%; Score 364.5; DB 4; Length 820;  
Best Local Similarity 30.4%; Pred. No. 3,4e-24;  
Matches 88; Conservative 43; Mismatches 115; Indels 43; Gaps 8;

QY 20 RPP--PEAPQRMRTMSHGRWPAGPHCAAVPEG-----DPPPLTMW 61  
Db 22 RSPFLPEQAQPW-----GAPVESEFLVHPGDLQLRCLRDYQSIINW 66  
QY 62 TKDGRTHSGMSRRVLPQGLKQVEREDAGVYVCKATNGFSLVNTLVLDISPG 121  
Db 67 LRDGQLAES-NRTRIGEVEVODSVADSGLYACTSSPSGS-DITYFSVNSDALPS 124  
QY 122 KESLGDSSSGGQOE---DPAQOQWARPRTQPSKMRRTVIRPVGSSVRLCAVSGHPR 178  
Db 125 SEDDDDDSSSEKETDNTKPNVAPYWTSPKMEKLAHVPAAKTVKFCPSGTPNP 184  
QY 179 DITMKDDQALTRPE---AAEPKKKWTLSLKLRLPEDSGKYTCRVSNRAGAINATYKV 234  
Db 185 TLRLKNGKEF-KPDHRIGYKVRATWSIIMDSVPSDKGNTCIYENEGSINHYYQL 243  
QY 235 DVIOETRSKPVLTGTHPVNTVDEGGTTSFQCKVRSVYKVIOMLKRYE 283  
Db 244 DYERSPHRPLTQAGLPANKTVALGSNVEFMCKYSDPOPHIOMLKHIE 292  
RESULT 14  
PCT-US93-05703-2  
Sequence 2, Application PC/TUS9305703  
GENERAL INFORMATION:  
APPLICANT: Nova, Michael P.  
APPLICANT: Gonzalez, Ana-Maria  
APPLICANT: Baird, J. Andrew  
TITLE OF INVENTION: Process for Detection of Neoplastic  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 South Lasalle Street, Suite 900  
CITY: Chicago  
STATE: IL  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/05703  
FILING DATE: 19930614  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/900,646  
FILING DATE: 18-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 54655PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-552-1311  
TELEFAX: 619-552-0095  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 351 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..351  
OTHER INFORMATION: /note="Sequence of  
OTHER INFORMATION: extracellular domain of an FGFR1"  
PCT-US93-05703-2

Query Match 20.3%; Score 360.5; DB 5; Length 351;  
Best Local Similarity 30.1%; Pred. No. 2,4e-24;  
Matches 86; Conservative 43; Mismatches 116; Indels 41; Gaps 7;  
QY 21 PPEPAPQRMRTMSHGRWPAGPHCAAVPEG-----DPPPLTMWTKD 64  
Db 2 PTLPEQAQPW-----GAPVESEFLVHPGDLQLRCLRDYQSIINLRD 46  
QY 65 GRTTHSGMSRRVLPQGLKQVEREDAGVYVCKATNGFSLVNTLVLDISPGES 124  
Db 47 GVLQALAES-NRTRIGEVEVODSVADSGLYACTSSPSGS-DITYFSVNSDALPS 104  
QY 125 LQPDSSSGGQOE---DPAQOQWARPRTQPSKMRRTVIRPVGSSVRLCAVSGHPR 181  
Db 105 DDDDDSSSEKETDNTKPNVAPYWTSPKMEKLAHVPAAKTVKFCPSGTPNP 164  
QY 182 WMKDDQALTRPE---AAEPKKKWTLSLKLRLPEDSGKYTCRVSNRAGAINATYKV 237  
Db 165 WLKNGKEF-KPDHRIGYKVRATWSIIMDSVPSDKGNTCIYENEGSINHYYQL 223  
QY 238 QRTSKRPVLTGTHPVNTVDEGGTTSFQCKVRSVYKVIOMLKRYE 283  
Db 224 ERSPHRPLTQAGLPANKTVALGSNVEFMCKYSDPOPHIOMLKHIE 269  
RESULT 15  
US-07-640-029-2  
Sequence 2, Application US/07640029  
Patent No. 5229501  
GENERAL INFORMATION:  
APPLICANT: Kiefer, Michael C.  
APPLICANT: Valenzuela, Pablo D.T.  
APPLICANT: Barr, Philip J.  
TITLE OF INVENTION: Expression and Use of Human Fibroblast  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/640,029  
FILING DATE: 19910111  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: McClung, Barbara G.  
REGISTRATION NUMBER: 33,113  
REFERENCE/DOCKET NUMBER: CH-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-655-3542  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 817 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-640-029-2

Query Match 20.3%; Score 360.5; DB 1; Length 817;  
Best Local Similarity 29.9%; Pred. No. 7.6e-24;  
Matches 87; Conservative 45; Mismatches 114; Indels 45; Gaps 8;



Db 125 SEDDDDDSSSEKETDNTKPNMPPVAPYWTSEKMEKKLHAVPAKTYKFKCPSSGTP 184  
QY 177 RPDITWKKDOALTRPE----AAEPKKKWTLSLKNLRPEDSGKYTCRVSNRGA1NATY 232  
Db 185 NPTLRMLKKNKEF-KPDHRIGGYKVRATWSIIMDSVPSDKGNVCIYENEXG5INHYY 243  
QY 233 KVDVIOQTRSKPVLGTGHPVNTVDFGTTSFQCKVRSQVDPKPYIOMLKRYE 283  
Db 244 QLDVVERSPHPIILQAGLPANKTYVALG5NVEFKCKYISDPQPHIOMLKHE 294

## RESULT 18

US-08-441-944A-4  
; Sequence 4, Application US/08441944A  
; Patent No. 5767250  
; GENERAL INFORMATION:  
; APPLICANT: SPAETE, RICHARD  
; TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CHIRON CORPORATION  
; STREET: 4560 Horton Street - R440  
; CITY: Emeryville  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94608-2916  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,944A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 530  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 07/921,807  
; FILING DATE: 29-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MCCLUNG, BARBARA G.  
; REGISTRATION NUMBER: 33,113  
; REFERENCE/DOCKET NUMBER: 0209,001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 601-2708  
; TELEFAX: (510) 655-3542  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 822 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-441-944A-4

Query Match 20.3%; Score 360.5; DB 1; Length 822;  
Best Local Similarity 29.9%; Pred. No. 7.7e-24;  
Matches 87; Conservative 45; Mismatches 114; Indels 45; Gaps 8;

QY 20 RPP--PEAPQWRTRMSHGKMPAGPHCAAAVVEG-----DPPPLTMW 61  
Db 22 RSPPTLPEQAQFW-----GAPVEVESFLVHPGDLQLRCRLRDDVQ5INW 66  
QY 62 TDDGRTHSGMSRFVLPQGLKVKOVEREDAGYVCATNGSGT5VNTLVLDISPG 121  
Db 67 LNDGVQLAES-NKRTITGEVEVD5VPAD5GLYACVT5SPG5-DITYFSVNSDALPS 124  
QY 122 KSLSPDSSSGQEDPA-----SQQWAPRFTQPSKMRRTVARIAPYSSVRLKCVASGHP 176  
Db 125 SDDDDDDSSSEKETDNTKPNRMPVAPYWTSEKMEKKLHAVPAKTYKFKCPSSGTP 184

QY 177 RPDITWKKDOALTRPE----AAEPKKKWTLSLKNLRPEDSGKYTCRVSNRGA1NATY 232  
Db 185 NPTLRMLKKNKEF-KPDHRIGGYKVRATWSIIMDSVPSDKGNVCIYENEXG5INHYY 243  
QY 233 KVDVIOQTRSKPVLGTGHPVNTVDFGTTSFQCKVRSQVDPKPYIOMLKRYE 283  
Db 244 QLDVVERSPHPIILQAGLPANKTYVALG5NVEFKCKYISDPQPHIOMLKHE 294

## RESULT 19

US-08-451-822A-12  
; Sequence 12, Application US/08451822A  
; Patent No. 5863888  
; GENERAL INFORMATION:  
; APPLICANT: Dionne, Craig A  
; APPLICANT: Crumley, Greg  
; APPLICANT: Jaye, Michael C  
; APPLICANT: Schlessinger, Joseph  
; TITLE OF INVENTION: Fibroblast Growth Factor Receptors  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Legal Department  
; STREET: 500 Atcola Road  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/451,822A  
; FILING DATE: 26-MAY-1995  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/323,430  
; FILING DATE: 14-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/934,372  
; FILING DATE: 21-AUG-1992  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 07/549,587  
; FILING DATE: 06-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A0496E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3816  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 822 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-451-822A-12

Query Match 20.3%; Score 360.5; DB 2; Length 822;  
Best Local Similarity 29.9%; Pred. No. 7.7e-24;  
Matches 87; Conservative 45; Mismatches 114; Indels 45; Gaps 8;

QY 20 RPP--PEAPQWRTRMSHGKMPAGPHCAAAVVEG-----DPPPLTMW 61  
Db 22 RSPPTLPEQAQFW-----GAPVEVESFLVHPGDLQLRCRLRDDVQ5INW 66  
QY 62 TDDGRTHSGMSRFVLPQGLKVKOVEREDAGYVCATNGSGT5VNTLVLDISPG 121  
Db 67 LNDGVQLAES-NKRTITGEVEVD5VPAD5GLYACVT5SPG5-DITYFSVNSDALPS 124



Db 125 SEDDDDDSSSEKETDNTKPNRPVAPYWTSPKMEKTLHAPPAKTVKFCPSGCT 184  
QY 177 RPDITWMDKDALTRPE---AAEPKKKWTLSIKNLRPEDSGKTCVRNAGAINFY 232  
Db 185 NPTLRMLKNGKEF-KPDHIGIKYKRYATWSIIMDSVSPSKGNTCTIVENYGSINHTY 243  
QY 233 KVDVIQRTSRKPVLTGTHPVNTVDGCTTSFQCKVRSDVAPVIOMLKRV 283  
Db 244 QLDVVERSPHRILOAGLPANKTVALGSNVEFMCKVYSDPQHIOMLKHIE 294

## RESULT 22

US-09-383-586-30  
; Sequence 30, Application US/09383586  
; Patent No. 6242419  
; GENERAL INFORMATION:  
; APPLICANT: Strachan, Lorna  
; APPLICANT: Sleeman, Matthew  
; APPLICANT: Abernethy, Nevin  
; APPLICANT: Onrust, Rene  
; APPLICANT: Mumble, Anand  
; APPLICANT: Murison, Greg  
TITLE OF INVENTION: Compounds isolated from stromal cells  
TITLE OF INVENTION: and methods for their use  
FILE REFERENCE: 11000.1037c1  
CURRENT APPLICATION NUMBER: US/09/383.586  
CURRENT FILING DATE: 1999-08-26  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 30  
LENGTH: 126  
TYPE: PRT  
ORGANISM: Mouse  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: (123)...(123)  
US-09-383-586-30

Query Match 19.7%; Score 350; DB 4; Length 126;  
Best Local Similarity 97.0%; Pred. No. 5.3e-24;  
Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 256 VDRGTTSFQCKVRSDVAPVIOMLKRVYAGRHNSSTIDVGCGKTVLPTGDWSPDG 315  
Db 1 VDRGTTSFQCKVRSDVAPVIOMLKRVYAGRHNSSTIDVGCGKTVLPTGDWSPDG 60  
QY 316 SYLNKPL 322  
61 SYLNKLL 67

## RESULT 23

US-08-166-717D-6  
; Sequence 6, Application US/08166717D  
; Patent No. 5789182  
; GENERAL INFORMATION:  
; APPLICANT: Yayon, Avner  
; APPLICANT: Ornitz, David M.  
; APPLICANT: Klagsbrun, Michael  
; APPLICANT: Leder, Philip  
TITLE OF INVENTION: SYSTEM FOR ASSAYING BINDING  
TITLE OF INVENTION: TO A HEPARIN-BINDING GROWTH  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM COMPATIBLE  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WordPerfect (Version 7.0)  
CURRENT APPLICATION NUMBER:  
APPLICATION NUMBER: US/08/166,717D  
FILING DATE: 12/14/93  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/631,717  
FILING DATE: 12/20/90  
ATTORNEY/AGENT INFORMATION:  
NAME: Kristina Bieker-Brady  
REGISTRATION NUMBER: 39,109  
REFERENCE/DOCKET NUMBER: 00383/017002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 723-4123  
TELEFAX: (617) 723-8962  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 820  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-166-717D-6

Query Match 19.6%; Score 349.5; DB 1; Length 820;  
Best Local Similarity 30.5%; Pred. No. 7.3e-23;  
Matches 89; Conservative 42; Mismatches 112; Indels 49; Gaps 10;

QY 20 RPPF--PEAPORMTWRSRHWAPGCAAAVPE-----GDPPPLM----- 60  
Db 22 RPAFLPEQAQPW-----GPEVESLIVHPGDLQLCRRLRDVOST 64  
QY 61 -WTKDG-RTHSGWSRFRVLPOGLKQVEREDAGVYVCKATNGFSLSYNTLVVLDI 118  
Db 65 NMXXDGQVLES--NRRTIGEEVEVDSPADSGLACTSSPSG-DITYSVANSDA 121  
QY 119 SPKESIGPPSSGGQE--DPAQOWARFTOPSKMRRTYARPYGSSVRLKCAVSGH 175  
Db 122 LPSEDDDDHDSSEKETDNTKPNRPVAPYWTSPKMEKTLHAPPAKTVKFCPSGCT 181  
QY 176 RPDITWMDKDALTRPE---AAEPKKKWTLSIKNLRPEDSGKTCVRNAGAINFY 231  
Db 182 NPTLRMLKNGKEF-KPDHIGIKYKRYATWSIIMDSVSPSKGNTCTIVENYGSINHT 240  
QY 232 YKVDVIQRTSRKPVLTGTHPVNTVDGCTTSFQCKVRSDVAPVIOMLKRV 283  
Db 241 QLDVVERSPHRILOAGLPANKTVALGSNVEFMCKVYSDPQHIOMLKHIE 292

## RESULT 24

US-07-640-029-5  
; Sequence 5, Application US/07640029  
; Patent No. 5229501  
; GENERAL INFORMATION:  
; APPLICANT: Kiefer, Michael C.  
; APPLICANT: Valenzuela, Pablo D.T.  
; APPLICANT: Barr, Philip J.  
TITLE OF INVENTION: Expression and Use of Human Fibroblast  
TITLE OF INVENTION: Growth Factor Receptor  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: California  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/640,029  
FILING DATE: 19910111  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: McClung, Barbara G.  
REGISTRATION NUMBER: 33,113  
REFERENCE/DOCKET NUMBER: CH-165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2708  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-640-029-5

Query Match 17.3%; Score 308; DB 1; Length 300;  
Best Local Similarity 35.6%; Pred. No. 9.2e-20;  
Matches 62; Conservative 30; Mismatches 74; Indels 8; Gaps 3;  
QY 117 DISPKESLGPDSSSGGQ---DPASQOARPRFTOPSKMRRIYARPVGSSVRLKCVAS 173  
DB 31 DALPSEDDDDDDSSSEKETDNTKPNPVA PYWTSPEKMEKHLAVPAKTVKFCPS 90  
QY 174 GHPREDITWKKDDQALTRPE---AAERPKKKWTLSLKNLPEDSGKTYTCRYSNAGALN 229  
DB 91 GTPNPTLRLKNGKEF-KPDHRIGYKVRYATWSLIMDSVPSDKGNTTCIYENEGYSIN 149  
QY 230 ATYKVDVIQRTSRKPVLTGTHPVNTTVDFGGTTSFQCKYRSDVKPVYIOMLKRE 283  
DB 150 HTYQLDVVERSPHRILOAGLPANKTVALGSNVERMCKVYSDPPHIOMLKHIE 203

RESULT 25  
US-08-439-992A-5  
Sequence 5, Application US/08439992A  
Patent No. 6255454  
GENERAL INFORMATION:  
APPLICANT: Kiefer, Michael C.  
APPLICANT: Pablo, Valenzuela D.T.  
APPLICANT: Philip, Barr J.  
TITLE OF INVENTION: Expression and Use of Human Fibroblast  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,992A  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Chung, Ling-fong  
REGISTRATION NUMBER: 36,482  
REFERENCE/DOCKET NUMBER: 0165, 004  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 510-923-2704  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 300 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-439-992A-5

Query Match 17.3%; Score 308; DB 4; Length 300;  
Best Local Similarity 35.6%; Pred. No. 9.2e-20;  
Matches 62; Conservative 30; Mismatches 74; Indels 8; Gaps 3;  
QY 117 DISPKESLGPDSSSGGQ---DPASQOARPRFTOPSKMRRIYARPVGSSVRLKCVAS 173  
DB 31 DALPSEDDDDDDSSSEKETDNTKPNPVA PYWTSPEKMEKHLAVPAKTVKFCPS 90  
QY 174 GHPREDITWKKDDQALTRPE---AAERPKKKWTLSLKNLPEDSGKTYTCRYSNAGALN 229  
DB 91 GTPNPTLRLKNGKEF-KPDHRIGYKVRYATWSLIMDSVPSDKGNTTCIYENEGYSIN 149  
QY 230 ATYKVDVIQRTSRKPVLTGTHPVNTTVDFGGTTSFQCKYRSDVKPVYIOMLKRE 283  
DB 150 HTYQLDVVERSPHRILOAGLPANKTVALGSNVERMCKVYSDPPHIOMLKHIE 203

Search completed: May 2, 2002, 08:50:20  
Job time: 122 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 2, 2002, 08:50:04 ; Search time 26.54 Seconds  
(without alignments)  
1774.668 Million cell updates/sec

Title: ~~US09823-038A-33~~  
Perfect score: 1779  
Sequence: 1 RRAAPCCSCRCRCRCMPSHR.....VLPTGDWNRPDSTYLNKPL 322

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%  
Listing first 100 summaries

Database :

SPRMBM1779  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1448	81.4	497	4 Q9BXN7	Q9BXN7 homo sapien
2	1448	81.4	504	4 Q9HAB7	Q9HAB7 homo sapien
3	401	22.5	822	13 Q91288	Q91288 pleurodeles
4	396.5	22.3	802	13 Q42127	Q42127 xenopus lae
5	393	22.1	800	13 Q918X3	Q918X3 brachydanio
6	391.5	22.0	800	4 Q99052	Q99052 homo sapien
7	387.5	21.8	446	11 Q63236	Q63236 rattus norv
8	387	21.8	800	11 Q9JHX9	Q9JHX9 rattus norv
9	386	21.7	824	13 Q90749	Q90749 rattus norv
10	384.5	21.6	822	11 Q9QVY7	Q9QVY7 gallus gall
11	384	21.6	796	13 Q91287	Q91287 pleurodeles
12	383.5	21.6	446	11 Q63237	Q63237 rattus norv
13	382.5	21.5	705	4 Q14718	Q14718 homo sapien
14	379	21.3	818	13 Q9PSV9	Q9PSV9 xenopus lae
15	378.5	21.3	810	13 Q9PS96	Q9PS96 xenopus lae
16	378.5	21.3	828	13 Q9DGK3	Q9DGK3 xenopus lae
17	377	21.2	818	13 Q91742	Q91742 xenopus lae
18	377	21.2	829	13 Q9PSV8	Q9PSV8 xenopus lae
19	376.5	21.2	357	6 Q18872	Q18872 sus scrofa

20	375.5	21.1	366	4 Q12922	Q12922 homo sapien
21	375.5	21.1	768	4 Q9UIH3	Q9UIH3 homo sapien
22	375.5	21.1	771	4 Q9UIH5	Q9UIH5 homo sapien
23	375.5	21.1	817	4 Q9UIH4	Q9UIH4 homo sapien
24	375.5	21.1	819	4 Q9UIH8	Q9UIH8 homo sapien
25	375.5	21.1	819	4 Q9UIH7	Q9UIH7 homo sapien
26	375.5	21.1	822	4 Q14672	Q14672 homo sapien
27	375.5	21.1	830	4 Q9UIH6	Q9UIH6 homo sapien
28	374	21.0	828	13 Q91743	Q91743 xenopus lae
29	368.5	20.7	814	13 Q91897	Q91897 xenopus lae
30	365	20.5	782	11 Q61563	Q61563 mus musculus
31	364.5	20.5	822	6 Q9T723	Q9T723 oryctolagus
32	364.5	20.5	822	11 Q60818	Q60818 mus musculus
33	363	20.4	480	13 Q9PSD1	Q9PSD1 xenopus . fl
34	362	20.3	480	13 Q9PSC9	Q9PSC9 xenopus . fl
35	361.5	20.3	662	4 Q02063	Q02063 homo sapien
36	360.5	20.3	922	13 Q90413	Q90413 brachydanio
37	356.5	20.0	360	11 Q61565	Q61565 mus musculus
38	356.5	20.0	361	11 Q9QW79	Q9QW79 mus sp. fib
39	356.5	20.0	824	13 Q91286	Q91286 pleurodeles
40	355.5	20.0	820	11 Q00389	Q00389 mus musculus
41	354	19.9	816	13 Q91285	Q91285 pleurodeles
42	353.5	19.9	376	11 Q9QW78	Q9QW78 mus sp. fib
43	328	18.4	357	11 Q63238	Q63238 rattus norv
44	327.5	18.4	724	13 Q03836	Q03836 xenopus lae
45	326	18.3	972	5 Q26614	Q26614 strongyloce
46	324	18.2	353	11 Q63242	Q63242 rattus norv
47	319	17.9	877	5 Q6GSH3	Q6GSH3 halocynthia
48	315	17.7	713	13 Q90330	Q90330 coturnix co
49	313	17.6	268	6 Q46603	Q46603 sus scrofa
50	310	17.4	395	13 Q9PSD0	Q9PSD0 xenopus . fl
51	309	17.4	279	4 Q9UD50	Q9UD50 homo sapien
52	308	17.3	300	4 Q14307	Q14307 homo sapien
53	308	17.3	707	6 Q9T070	Q9T070 canis famli
54	308	17.3	733	11 Q9Q2M7	Q9Q2M7 mus musculus
55	307	17.3	331	11 Q63239	Q63239 rattus norv
56	307	17.3	729	11 Q63827	Q63827 rattus norv
57	305	17.1	733	11 Q60830	Q60830 mus musculus
58	304	17.1	302	4 Q14306	Q14306 homo sapien
59	304	17.1	705	11 Q63710	Q63710 rattus norv
60	302	17.0	242	6 Q46604	Q46604 sus scrofa
61	302	17.0	330	11 Q63241	Q63241 rattus norv
62	294	16.5	287	11 Q9QW80	Q9QW80 mus sp. fib
63	294	16.5	671	11 Q63711	Q63711 rattus norv
64	282.5	15.9	729	13 Q91147	Q91147 notophthalm
65	282.5	15.9	650	11 Q91150	Q91150 notophthalm
66	282	15.9	731	13 Q63709	Q63709 rattus norv
67	272.5	15.3	201	6 Q9BGC9	Q9BGC9 macaca fasc
68	268	15.1	192	11 Q9ERP7	Q9ERP7 rattus norv
69	264	14.8	202	11 Q9ERP6	Q9ERP6 rattus norv
70	257	14.4	257	4 Q14719	Q14719 homo sapien
71	256	14.4	2037	5 Q9V1S8	Q9V1S8 drosophila
72	254	14.3	1675	13 Q9BSW4	Q9BSW4 brachydanio
73	245	13.8	2828	4 Q9NR99	Q9NR99 homo sapien
74	243.5	13.7	1052	5 Q9YUC8	Q9YUC8 drosophila
75	240	13.5	1380	4 Q9HCK4	Q9HCK4 homo sapien
76	237	13.3	1612	11 Q89026	Q89026 mus musculus
77	237	13.2	1651	4 Q9Y6N7	Q9Y6N7 homo sapien
78	235	13.2	1094	4 Q9BYB8	Q9BYB8 homo sapien
79	234.5	13.2	483	4 Q9UF14	Q9UF14 homo sapien
80	234	13.2	1395	5 Q9W213	Q9W213 drosophila
81	233	13.1	423	5 P91572	P91572 caenorhabdi
82	233	13.1	1273	5 Q44928	Q44928 caenorhabdi
83	233	13.1	1395	5 Q44924	Q44924 drosophila
84	232.5	13.1	1060	11 Q9Q213	Q9Q213 rattus norv
85	232.5	13.0	5198	5 Q76518	Q76518 caenorhabdi
86	231.5	13.0	1342	5 Q9GPP6	Q9GPP6 drosophila
87	230.5	13.0	946	13 Q07153	Q07153 torpedo cal
88	230	12.9	1406	5 Q9GPP7	Q9GPP7 drosophila
89	230	12.9	1496	4 Q92626	Q92626 homo sapien
90	226.5	12.7	823	5 Q9V010	Q9V010 rattus norv
91	226.5	12.7	823	5 Q9V010	Q9V010 drosophila
92	226.5	12.7	4370	4 Q9H3V5	Q9H3V5 homo sapien

93 221.5 12.5 729 5 09VED5 09ved5 drosophila  
 94 220 12.4 1344 11 09Z214 09z214 mus musculu  
 95 219.5 12.3 555 4 09U0H8 09ugh8 homo sapien  
 96 219 12.3 2174 5 09GCR0 09gcr0 drosophila  
 97 218.5 12.3 1033 5 09V643 09v643 drosophila  
 98 218.5 12.3 6642 5 001761 001761 caenorhabdi  
 99 216.5 12.2 163 13 093418 093418 gallus gall  
 100 215.5 12.1 554 4 09UQH9 09ugh9 homo sapien

## ALIGNMENTS

RESULT 1  
 09BXN7 PRELIMINARY; PRT; 497 AA.  
 AC 09BXN7;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DE FGF HOMOLOGOUS FACTOR RECEPTOR.  
 GN FHR.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Aggarwal S., Xie M.-H., Foster J., Frantz G., Stinson J., Corpuz R.T.,  
 RA Simmons L., Hillan K., Yansura D.G., Vandlen R.L., Goddard A.D.,  
 RA Gurney A.L.;  
 RT "FHR, a novel fibroblast growth factor receptor that uniquely binds  
 RT the fibroblast growth factor homologous factors";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF312678; AAK15273.1; -  
 KW Receptor.  
 SQ SEQUENCE 497 AA; 53757 MW; 57301F4F36357360 CRC64;

## Query Match

Best Local Similarity 81.4%; Score 1448; DB 4; Length 497;  
 Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 PVEGDPPPLMTMTKDGRTIHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGFGLSVN 109  
 |||||||  
 DB 52 PVEGDPPPLMTMTKDGRTIHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGFGLSVN 111  
 |||||||  
 QY 110 YTLVAVDDISPGRSLGPDSSSGQEDPASQOMARPRFTQPSKMRVRVIARPVGSSVRLK 169  
 |||||||  
 DB 112 YTLVAVDDISPGRSLGPDSSSGQEDPASQOMARPRFTQPSKMRVRVIARPVGSSVRLK 171  
 |||||||  
 QY 170 CVASGHRPDIITMMKDDQALTRPEAEPRKKMTLSLKNLRPDSGKYTCRVSNRAGAIN 229  
 |||||||  
 DB 172 CVASGHRPDIITMMKDDQALTRPEAEPRKKMTLSLKNLRPDSGKYTCRVSNRAGAIN 231  
 |||||||  
 QY 230 ATTKVDVIOIRTSKRPVLTGHPVNTIVDFGTTSFQCKVRSVDKPVYIOWIKRVEYGAEGR 289  
 |||||||  
 DB 232 ATTKVDVIOIRTSKRPVLTGHPVNTIVDFGTTSFQCKVRSVDKPVYIOWIKRVEYGAEGR 291  
 |||||||  
 QY 290 HNSTIDVGOKFVYLPFGDVWSRPDGSYLKPL 322  
 |||||||  
 DB 292 HNSTIDVGOKFVYLPFGDVWSRPDGSYLKPL 324  
 |||||||

## RESULT 2

09HAD7 PRELIMINARY; PRT; 504 AA.  
 AC 09HAD7;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE FGFRL1 OR FGFRL1  
 GN FGFRL1 OR FGFRL1

OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wiedemann M., Trued B.;  
 RT "Characterization of a novel protein (FGFRL1) from human cartilage  
 RT related to FGF receptors.";  
 RL Genomics 69: 275-279 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-21167383; PubMed-11267671;  
 RA Kim I., Moon S.O., Yu K.H., Kim U.H., Koh G.Y.;  
 RT "A novel fibroblast growth factor receptor-5 preferentially expressed  
 RT in the pancreas.";  
 RL Biochim. Biophys. Acta 1518:152-156(2001).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AJ277437; CAC14171.1; -  
 DR EMBL: AF279689; AAK26742.1; -  
 DR Interpro: IPR003599; Ig.  
 DR Interpro: IPR003598; Ig\_C2.  
 DR Interpro: IPR003600; Ig\_Like.  
 DR Interpro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig; 3.  
 DR SMART: SM00409; Ig; 3.  
 DR SMART: SM00408; IgC2; 3.  
 DR SMART: SM00410; Ig\_Like; 2.  
 KW Signal; Receptor.  
 FT SIGNAL 1 17 POTENTIAL.  
 SQ SEQUENCE 504 AA; 54567 MW; 16382E57D4276485 CRC64;

## Query Match

Best Local Similarity 81.4%; Score 1448; DB 4; Length 504;  
 Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 PVEGDPPPLMTMTKDGRTIHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGFGLSVN 109  
 |||||||  
 DB 52 PVEGDPPPLMTMTKDGRTIHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGFGLSVN 111  
 |||||||  
 QY 110 YTLVAVDDISPGRSLGPDSSSGQEDPASQOMARPRFTQPSKMRVRVIARPVGSSVRLK 169  
 |||||||  
 DB 112 YTLVAVDDISPGRSLGPDSSSGQEDPASQOMARPRFTQPSKMRVRVIARPVGSSVRLK 171  
 |||||||  
 QY 170 CVASGHRPDIITMMKDDQALTRPEAEPRKKMTLSLKNLRPDSGKYTCRVSNRAGAIN 229  
 |||||||  
 DB 172 CVASGHRPDIITMMKDDQALTRPEAEPRKKMTLSLKNLRPDSGKYTCRVSNRAGAIN 231  
 |||||||  
 QY 230 ATTKVDVIOIRTSKRPVLTGHPVNTIVDFGTTSFQCKVRSVDKPVYIOWIKRVEYGAEGR 289  
 |||||||  
 DB 232 ATTKVDVIOIRTSKRPVLTGHPVNTIVDFGTTSFQCKVRSVDKPVYIOWIKRVEYGAEGR 291  
 |||||||  
 QY 290 HNSTIDVGOKFVYLPFGDVWSRPDGSYLKPL 322  
 |||||||  
 DB 292 HNSTIDVGOKFVYLPFGDVWSRPDGSYLKPL 324  
 |||||||

## RESULT 3

091288 PRELIMINARY; PRT; 822 AA.  
 AC 091288;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE FIBROBLAST GROWTH FACTOR RECEPTOR.  
 OS Pleurodeles waltlilii (Iberian ribbed newt).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae;  
 OC Pleurodeles.

OX	NCBI_TaxID=8319;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=93130775; PubMed=1483392;
RX	Shi D.L., Feste J.J., Riou J.E., Boucaut J.C.;
RT	Differential expression and regulation of two distinct fibroblast
RT	growth factor receptors during early development of the urodele
RT	amphibian <i>Pleurodeles waltl</i> ."
RL	Development 116:261-273(1992).
CC	-1. SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC	DOMAIN.
DR	EMBL: X65059; CAA46192.1; "
DR	HSSP: P06239; 3lCk.
DR	InterPro: IPR000719; Euk_pkinase.
DR	InterPro: IPR003598; Ig_c2.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR001245; Tyr_kin.
DR	Pfam: PF00047; Ig_3.
DR	Pfam: PF00069; pkinase. 1.
DR	PRINTS: PR00109; TYRKINASE.
DR	SMART: SM00408; IGC2_3.
DR	SMART: SM00219; TYKc; 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
DR	PROSITE: PS00109; PROTEIN_KINASE_TYR. 1.
QW	ATP-binding, Transferase; tyrosine-protein kinase.
QV	SEQUENCE 822 Aa; 92068 MW; 3EC4BA4B9C9AB18A CRC64;

QY	61	WTEDGRTTISGWARFENVLPQGLVKQVREDDACVYCAKATNGGSLSVNTLVLLDISP	120
Db	80	YTESLHOGHG--RIILFTDVLTEIADVLYEDSLYLIC-VYPGCHILIRNFTISVDSIAS	136
QY	121	G---KSLGPDSSG--GOEDPASQOMARPRFTQPSKMRRTIARPVGSSVRLCYASGH	175
Db	137	GDDDDHDHGEDSAGIMGEDPRYSTYSRAFWGQOPORMKKLTAVPAGNTVVKRCPSAGN	196
QY	176	PREDITFMKDDOL--TPREAEPKKKWITLSKMLRPEDSCSKYCRVSNRAGALNATY	232
Db	197	PTGIGIMLKNGRFGEGEHRIGGIRLRHOKHSLMYESVSPDRGNITCYLVENKFGSISYST	256
QY	233	KVDVIQRTSKPVLSTGHPYNTIVDEGGTTSFOCKVRSIDKPYVIMLKRVE-----YGAE	287
Db	257	LIDVLEERSPPRIQLAGLRANTTAMLGSDVQFCYKYSDAQPIHQMKNHEVGNRGRPD	316
QY	288	G-----RHNSITDYGGOKFVYLPRLPGDYWSRPRDGSY	317
Db	317	GVPEYQVLATADINSSEVELLYLHNVSFEDAGEY	350

CC	RESULT	4
CC	042127	
AC	042127	PRELIMINARY: PRT: 802 AA.
DT	01-JAN-1998	(TREMBLrel. 05, Created)
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)
DE		FGF RECEPTOR 3.
OS		Xenopus laevis (African clawed frog).
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC		Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC		Xenopodinae; Xenopus.
OX		NCBI_TaxID=8355;
RN		[1]
RP		SEQUENCE FROM N.A.
RA		Hongo I., Kengaku M., Okamoto H.;
RA		Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC	-i-	SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.

Query Match	22.3%	Score 396.5	DB 13	Length 802
Similarity	32.9%	Pred. No. 7.1e-26		
Best Local	49	Mismatches 98	Indels 45	Gaps 9

QY	45	CAAAVEEGPPPLTMMTKGRTIHSGRSFRVPL	-----0G-LTKVKVEREDAGVY	96
Db	52	CAAE-----DASTTKKCKRG	-----IGIVPNNRSTRGCLKIIIVSSDDSGITS	97
QY	97	CKATNGFGLSVNTLVLLDDISBPKESLCPDSSSGGQEDPASQOQMARPRETOPSKMRR	156	
Db	98	CRMHSTEILR-NFTIIVTD-----LPSSGDEDDDDDDDEDEDREPRPMTOPPERMEK	151	
QY	157	VIAWPVSVRLKCVASGHPRPDITWKKDDOALT---	RPAEPRKKKMTLSLKNLPED	213
QY	152	LIAPAANTLIRFCRPAAGNPPTIIHMLKNEKERRGEGHRIIGCIKIRHOOMSLWESVPSD	211	
Db	152	LIAPAANTLIRFCRPAAGNPPTIIHMLKNEKERRGEGHRIIGCIKIRHOOMSLWESVPSD	211	
QY	214	SGRYTCFVSRAQAINATYEVYDIQIOTRSKPVILGTHRPVNTTYDDFGTTSFOCKVRSDVK	273	
Db	212	KGNVTCEVNEKYSIRQTYQDVLERSHRPILQAGLPNGQTVJLGSDFVEHCKVYSDAQ	271	
QY	274	PVIQMLKRYEYGAERGRINSTIDVGGQCFVYLPFGDVMASRDGSLYN	319	
Db	272	PHIQMLKRYEYGAERGRINSTIDVGGQCFVYLPFGDVMASRDGSLYN	303	

	RESULT	5	
	Q918X3		
ID	Q918X3	PRELIMINARY;	PRT; 800 AA.
AC	Q918X3;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)		
DE	FIBROBLAST GROWTH FACTOR RECEPTOR 3. FGFR3.		
GN	Brachydanio rerio (zebrafish) (Zebra danio).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasbora; Danio.		
OC	NCBI_TaxId=7955;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	Slepsova-Friedrich I., Li Y., Korzh V., Ge R.; "The zebrafish fibroblast growth factor receptor 3 (z-FGFR3) in early zebrafish development.";		
RA	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
RT	-I- SIMILARITY: TO IMMUGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX		
RL	DOMAIN:		
CC	EMBL; AF157560; AAF80344.1; -;		
CC	InterPro; IPR000719; Euk_pkinase.		
CC	InterPro; IPR003598; Ig_c2.		
CC	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR001245; Tyr_kin.		
DR	Plan; PF000047; Ig_3.		



RX MEDLINE-93326167; PubMed-6333865;  
 RA Yan G., McBride G., McKeenan W.L.;  
 RT "Exon skipping causes alteration of the COOH-terminus and deletion of  
 RT the phospholipase C gamma 1 interaction site in the FGF receptor 2  
 RT kinase in normal prostate epithelial cells.";  
 RL Biochem. Biophys. Res. Commun. 194:512-518(1993).  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: L19104; AAA02629.2; -.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig; 3.  
 DR SMART: SM00408; IGC2; 3.  
 KM Receptor.  
 FT NON\_TER 1 1  
 FT 446 446  
 SQ SEQUENCE 446 AA; 49379 MW; 276DF304DD3080E3 CRC64;

Query Match 21.8%; Score 387.5; DB 11; Length 446;  
 Best Local Similarity 30.5%; Pred. No. 2.1e-25;  
 Matches 99; Conservative 53; Mismatches 133; Indels 37; Gaps 9;

QY 23 PPEAPQMRTRMSHGRMPAGPHCAAAVPEG-----DPEPLTMWTKDGRTHSGMSRF 75  
 Db 62 PEEPTKYQI-----SQEACVAVPAGESLELRCMLKDAAVLSWTKDG--VHLGPNR 111  
 QY 76 RVL-PQGLKAVQREDAGVYVCATNGFSGLSVNTLVLDISPGKESGPDSSGCG 134  
 Db 112 TLVLEGIQIIGANPRPSGLYCAAAARTVDESETLYFMVNTVDAISGDEDEDTSSSEDFV 171  
 QY 135 EDPAQOQWAPRFTQPSKMRRTVARIAPGSSVRLKCVASGHPRDIIMMKDQALT--R 191  
 Db 172 SENSNOBA-PYWNTEMEKRLHAVPAANTVVKRCRPGGMPPTMRMLKNGKEKOEHR 230  
 QY 192 PEAAPRRKKWTLSLKLPEDSGYTCRVSNRAGAINATKYVDIORTSKPVLTGTHP 251  
 Db 231 IGVKRVNRQHSILMESVPSDKNTCYLVENEGSINHITHLDVNESPHRPLQAGLP 290  
 QY 252 VNTTVDEGGTTSFOCKYRSDVKPYIOWLKRYE-----YGAGC-----RHNSITDVGCG 299  
 Db 291 ANASTVVGDEYFCKYVSDAOPHIOWIKHEKNGSKYGPDLRYLKLKHS---INSS 347  
 QY 300 KFYVLPFGDVMSRPGSYLNK 320  
 Db 348 NAEVLALFNVTEDAGEYICK 368

RESULT 8  
 Q9JHX9 PRELIMINARY; PRT; 800 AA.  
 AC Q9JHX9;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE FIBROBLAST GROWTH FACTOR RECEPTOR 3.  
 GN FGR3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HANOVER WISTAR;  
 RA Claus P., Grothe C.;  
 RT "Molecular Cloning and Developmental Expression of Rat Fibroblast  
 RT Growth Factor Receptor 3 (FGR3)."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
 CC DOMAIN.  
 DR EMBL: AF277717; AAF97795.1; -.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003598; Ig\_c2.

DR InterPro: IPR003600; Ig\_like.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR001245; Tyr\_kin.  
 DR Pfam: PF00047; Ig; 3.  
 DR Pfam: PF00069; pkinase.1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; IGC2; 2.  
 DR SMART: SM00410; IG\_Like; 1.  
 DR SMART: SM00219; TyrcK; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 KM ATP-binding; Receptor; Tyrosinase; Tyrosine-protein kinase.  
 SQ SEQUENCE 800 AA; 87674 MW; 128C838A2B990031 CRC64;

Query Match 21.8%; Score 387; DB 11; Length 800;  
 Best Local Similarity 32.1%; Pred. No. 4.7e-25;  
 Matches 102; Conservative 49; Mismatches 133; Indels 34; Gaps 9;

QY 5 CCCSCRCRCGSPSHRPPPEAPQMRTRMSHGRMPAGPHCA-----AVPVGCD 54  
 Db 6 CVLVECVAVVAGVYSEPPGQVRGAAAEVPPESQEQVAFSGDPTVELSCHPPGA 65  
 QY 55 PEPPLMTWTKDGRTHSGMSRFRVL-PQGLKAVQREDAGVYVC--KATNGFSGLSVNTLV 112  
 Db 66 PTGPTLAKKDVGLVAS-HRLVGPORLOVLNATHEDAGVYSCQORLTR---RVLCHEFV 121  
 QY 113 VLLDISPGKESLPGDSSSGGDEDPASQOQWAPRFTQPSKMRRTVARIAPGSSVRLKCV 172  
 Db 122 RVTDA PSSGDEDEDGDA-----EDTGAPY-----TRPERMDKLLAVPANTVFERCPA 172  
 QY 173 SGHRPDIIMMKDQALT--RPEAEPKRRKKWTLSLKLPEDSGYTCRVSNRAGAIN 229  
 Db 173 AGNPTPSIPWLKNGKEFGRHIGIKLRHQOWSLMESVPSDKNTCYLVENEGFSGIR 232  
 QY 230 ATYKVDIORTSKPVLTGTHPNTTVDEGGTTSFOCKYRSDVKPYIOWLKRYEYAGAGR 289  
 Db 233 QTYTLDVYERSPHRPLIIOAGLPANQTAVLGSDVEFHCKYVSDAOPHIOWLKHAHEY----- 287  
 QY 290 HNSITDVGQREY-VLPT 306  
 Db 288 NGSKVGPDGTPYVTVLKT 305

RESULT 9  
 Q90749 PRELIMINARY; PRT; 824 AA.  
 AC Q90749;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
 DE RECEPTOR TYROSINE KINASE.  
 GN BEK.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91319411; PubMed-1650446;  
 RA Sato M., Kitazawa T., Iwai T., Seki J., Sakato N., Kato J.Y.,  
 RA Takeya T.;  
 RT "Isolation of chicken-bek and a related gene; identification of  
 RT structural variation in the ligand-binding domains of the FGF-receptor  
 RT family.";  
 RL Oncogene 6:1279-1283(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC Takeya T.;  
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX





CC DOMAIN.  
DR EMBL: X75603: CAA53271.1; -.  
DR HSPD; P06239; 3ICX.  
DR InterPro: IPR000719; Euk\_kinase.  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR001245; Tyr\_kin.  
DR Pfam: PF00047; Ig; 3.  
DR Pfam: PF00069; kinase; 1.  
DR PRINTS; PRO0109; TYRKINASE.  
DR SMART; SM00408; IGC2; 3.  
DR SMART; SM00219; TYKIC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR ATP-binding; Transferase; tyrosine-protein kinase.  
SO SEQUENCE 796 AA; 88288 MW; 226099A0B6DD1D92D CRC64;

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QY      60  MMTDKGRI-----HSGMSRFRLPOLQKQYVEREDAGYGVYKATNGFESTLVTLY  113
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      66  VMFKDGLSDVDPPTMSHG-----QRLKLIINSYDSSGVYSCKANQSSVYLK-NTYR  112

QY      114  VLDDISPKESLGDSSSGGGEPPASOOMANPRTQPSKMRRLVYIARVGSVYALKCYAS  173
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      118  VTD-----SPSSGDDEDDDEESANAPKTRTPMEKKLTLAPAAATVFFRCPA  166

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[illegible]

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QY      291 NSTIDVGQKFEVLLPTGDVWSRPDGS 316
          | | |
Db      282 -----VNGSKF-----GPDGN 292

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RESULT	12			
063237				
ID	063237	PRELIMINARY;	PRT;	446 AA.
AC	063237;			
DT	01-NOV-1996 (TREMBLrel, 01, Created)			
DT	01-NOV-1996 (TREMBLrel, 01, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel, 17, Last annotation update)			
DE	HEPARIN-BINDING FIBROBLAST GROWTH FACTOR RECEPTOR 2 (FRAGMENT).			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus			
NCBI_TaxId	10116;			
RNA	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PROSTATE;			
RX	MEDLINE=93326167; PubMed=8333865;			
RA	Yan G., McBride G., McKeenan W.L.;			
RT	"Exon skipping causes alteration of the COOH-terminus and deletion of			
RT	the phospholipase C gamma 1 interaction site in the FGF receptor 2			
RL	kinase in normal prostate epithelial cells.";			
RL	Biochem. Biophys. Res. Commun. 194:512-518(1993).			
CC	-I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLE			
CC	DOMAIN.			
EMBL	L19105; AAA02628.2; -			
DR	InterPro: IPR003598; Ig_c2.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	Pfam: PF00047; Ig_3.			
DR	SMART; SM00408; Igc2; 3.			
TM	Receptor.			

FT	NON_TER	446	446
SEQ	SEQUENCE	446 AA;	49249 MW; A8C3BFD1D7DBB123 CRC64

Query Match	21.6%	Score 383.5	DB 11	Length 446
Best Local Similarity	32.3%	Pred. No. 4.6e-25		
Matches 91	Conservative 48	Mismatches 116	Indels 27	Gaps 7

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OY      |   :    :       :     :  
23 PPEAPQMRWTRWSHGKWPAGPHCAAAPVEG-----DPPPLTMTWKDGRTIHSGSRF 75
```

QY 76 RVL-PQGLKVKQVEREDAGVYVCATNGFSLSYNYTLVLDDISPGEKESLGPDSSSGQ 134  
|| :|:| | :|:| | :  
Dh 113 EVITREVIOTGCAEMPECCIVNMAAEMRDESEMTVEAMUADATSCGDDEMDCESENV 172

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Oy 135 EDPASOOWARPREFTQPSKMRRIYARPVGSSVRLKCVASGHPRPDITWMKDOALT---R 191
      : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 173 SENRSQORA - PYWNTETKEMEKRLHAVPANTVVKFRCPAGAGNPTPIRMLKKNCKEFGQEH 231

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[illegible]

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Oy      252 VNTTDEGGTTSFQCKVRSDDVKPVIQWIKRVE-----YGAEG 288
      | : | | | | | : | | | | |
Db      292 ANASTVVGGVGFVFCVKVYSDAQPHIQWIKHVEKNGSKYGPDG 333

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RESULT	13	
014718		
ID	014718	PRELIMINARY;
		PRT; 705 AA

DT 01-NOV-1996 (TEMBLrel. 01, last sequence update)  
DT 01-JUN-2001 (TEMBLrel. 17, last annotation update)  
DE FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (FGFR-2) (EC 2.7.1.112)

OC *nono sapientia* (humanity);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID-9606;

RA Suji-mura T., Terada M.;  
RA Katoh M., Hattori Y., Sasaki H., Tanaka M., Sugano K., Yazaki Y.,  
RX MEDLINE=92212948; Pubmed=1313574;  
RP SEQUENCE FROM N.A.

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.

DR InterPro; IPR000719; Euk\_pkinase.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003006; Ig\_MHC.

DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR SMART; SM00408; TGC2; 2.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;

FT	RECEPTOR, SIGNAL, TRANSFERASE, TRANSMEMBRANE, TYROSINE KINASE
FT	SIGNAL
FT	CHAIN
FT	POTENTIAL.
FT	FIBROBLAST GROWTH FACTOR RECEPTOR 2.
FT	SEQUENCE
FT	705 AA; 79211 MW; 590967DCBFEDA25D CRC64;

```

Query Match      21.5%; Score 382.5; DB 4; Length 705;
Best Local Similarity 29.6%; Pred. No. 9,8e-25;
Matches 104; Conservative 52; Mismatches 130; Indels 65; Gaps 11;

OY 23 PPEAPQWRWRMSHGRNAPAGHCAAPVER-----DEPPLTMWTKDGTTHSGSRF 75
DB 35 PEEPTPTKYQI-----SOPEYVVAAPGESLEVRCLIKDAVAISWTKDG--VHLGNNR 84

OY 76 RVL-POGLKAYOVERDAGVVCATNGFGLSVNYTLIVLDDISPKESIGPSSSGGQ 134
DB 85 TVLIGETLQIKGATPRRSGILACTASRTVDSFTPMVNTDIAISSGD-----EDTDGA 140

OY 135 EDPASQ--QWAPRFTQPSKMRRTYIARPVSSVRLKCAVSGHPRDITWMDQALY 190
DB 141 EDFESENSNNKRAVPYNTTEMEKRLHAAPAANTVFRCPAGNPMPTMLRLKNGKEFKQ 200

OY 191 --PEAAEPKKKWTLSLKNLRPEDSGKTYTCRVSNRAGAINATYKVYIQTRSKPVLTG 248
DB 201 EHRIGGKIVKNQHSLSLMEVSPDSKNGNYTCVENEYGSINHTYTHDIVERSPHRPIIQA 260

OY 249 THPVNTVDFGTTSPQCKVRSVDPKPYIOMLKRYE-----YGAEG----- 288
DB 261 GLPANASTVVGDEYFCCKYSDAQPHIQWIKHEKNGSKYGGDGLPYLKVLSAESS 320

OY 289 -----RHNSTID---VGQKQVVLPTGVDWSPR-DGSLINKPL 322
DB 321 SANSNTPLVIRITRISTSTADTPMLAGVSEYLEDPEPKMEPRDKLTIGKPL 371

RESULT 14
OYPSV9 ID OYPSV9 PRELIMINARY; PRT; 818 AA.
AC OYPSV9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RGF RECEPTOR 4A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hongu I., Kengaku M., Okamoto H.;
RT "Differential employment of FGF signaling system for the embryonic
RT induction.";
RL Submitted (SEP-1987) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AB007036; BAA22849.1; -.
DR HSSP; P06239; 3LCK.
DR InterPro; IPR000719; Euk.pkinase.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001245; Tyr_kin.
DR Pfam; PF00047; Ig_3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TYRKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Receptor; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 818 AA; 92067 MW; A8CBA341C9230C1 CRC64;

Query Match      21.3%; Score 379; DB 13; Length 818;
Best Local Similarity 32.7%; Pred. No. 2,4e-24;
Matches 85; Conservative 46; Mismatches 87; Indels 42; Gaps 7;

OY 76 RVLPGQ-----LKVQVERDAGVVCATNGFGLSVNYTLIVLDDISPKESLGP 127

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DB 79 RLLPGKIRWGVGLEVDVTEYDSGLYIC-VVARGTKILRRSISVVDLSAGDEB--- 134
OY 128 DSSSGQEDPASQ-----QWAPRFTQPSKMRRTYIARPVSSVRLKCAVSGHPRPD 180
DB 135 DDEGREDTADINEPVEYFQAPVWTOPIHRMDKILHAAPAGNTVFRCPAGSGPLPTI 194
OY 181 TWMKDQALY--PEAAEPKKKWTLSLKNLRPEDSGKTYTCRVSNRAGAINATYKVYI 237
DB 195 RVLKNGEFGFGEHRIGIQIRHQSLSLMEVSPDSKNGNTCYENRVGSLTYTFLIDL 254
OY 238 QTRSKPVLNGTHPVNTVDFGTTSPQCKVRSVDPKPYIOMLKRYEYGAERHNSITDVG 297
DB 255 ERSRSHRPIIQAQPLPANTARVGSDEYFCVYSDAQPHIQWLKHE-----VN 302
OY 298 GQKF-----VLPPTGDV 309
DB 303 GSRFGPDPFPYVQLKTADI 322

RESULT 15
OYPSV9 ID OYPSV9 PRELIMINARY; PRT; 810 AA.
AC OYPSV9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FIBROBLAST GROWTH FACTOR RECEPTOR TYPE 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96032697; PubMed=7559402;
RX Gillespie L., Chen G., Paterno G.D.;
RT "Cloning of a fibroblast growth factor receptor 1 splice variant from
RT xenopus embryos that lacks a protein kinase C site important for the
RT regulation of receptor activity.";
J. Biol. Chem. 270:22758-22763(1995).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR HSSP; P06239; 3LCK.
DR InterPro; IPR000719; Euk.pkinase.
DR InterPro; IPR003598; Ig_C2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001245; Tyr_kin.
DR Pfam; PF00047; Ig_3.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00219; TYRKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 810 AA; 90294 MW; AC97B87BEEB1E72 CRC64;

Query Match      21.3%; Score 378.5; DB 13; Length 810;
Best Local Similarity 33.7%; Pred. No. 2,6e-24;
Matches 87; Conservative 51; Mismatches 101; Indels 19; Gaps 8;

OY 61 WKDGTTHSGSRFRVLDQGLKVOVERDAGVVCATNGFGLSVNYTL---VLLDD 117
DB 65 WYKNGVOL-SENNRTRITGEIIOISNAGPEDNGVYAC-VTNG---PSRTYVLFYSVNSD 119
OY 118 ISPKESLGPSSSGQEDPASQWNA--RPRFTQPSKMRRTYIARPVSSVRLKCAVSGH 175
DB 120 ALPSAEDDEDNDSSEKAAENSKPNRPLWSHPKMKKILHAAPAANTVFRCPAGNT 179
OY 176 PRDITWMDQALYRPE--AAEPKKKWTLSLKNLRPEDSGKTYTCRVSNRAGAINATY 232

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Db 180 PTLPLMKNKNGRAFOQDORIGYKRVSTWMLINDSVPSDKNGTTCVENEKKAINTTY 239
Oy 233 KVDVYIORTSKRPVLTGTHPVNTVDFGGTTSFOCKYRSDVKPVYIOMLKREYGAERHNS 292
Db 240 QLDVVERSPHPIIQAAGLPANTSVTGTAFFSCKYSDPOPHIOMLRHIE-----NGS 294
Oy 293 TIDVGOKFV-VLPTGDV 309
Db 295 RVASDGFPEYELKTAGV 312

RESULT 16
09DCK3 PRELIMINARY; PRT: 828 AA.
AC 09DCK3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FIBROBLAST GROWTH FACTOR RECEPTOR 4C.
GN FGFR-4C.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11180841;
RA Golub R., Adelman Z., Clement J., Weiss R., Bonasera J.,
RA Servetnick M.;
RT "Evolutionarily conserved and divergent expression of members of the
RT FGF receptor family among vertebrate embryos, as revealed by FGFR
RT expression patterns in Xenopus."
RL Dev. Genes Evol. 210:345-357(2000).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF288453; AAG01013.1; -.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00047; Ig; 3.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00409; IG; 3.
DR SMART: SM00408; IGG2; 3.
DR SMART: SM00410; IG_Like; 2.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYRKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding: Receptor; Transferrase
KW SEQUENCE 828 AA; 93211 MW; 72E2052635D5E323 CRC64;
SO

Query Match 21.3%; Score 378.5; DB 13; Length 828;
Best Local Similarity 32.5%; Pred. No. 2,7e-24;
Matches 86; Conservative 51; Mismatches 103; Indels 25; Gaps 8;
```

```
Db 195 PAGSPPLTIMKNGRFRGEHRIGIQIRHQHSLMESVSPSDRGNTCVENRYGS 254
Oy 228 INATYKVDVYIORTSKRPVLTGTHPVNTVDFGGTTSFOCKYRSDVKPVYIOMLKREYGAE 287
Db 225 LTYTFYDLVERSSHRPILQAAGLPANTSVTGTAFFSCKYSDPOPHIOMLRHIE--VN 312
Oy 288 GRHNSTIDVGOKF--VVLPTGDV 309
Db 313 GSH-----FGPDFFPYVYVLTADT 332

RESULT 17
091742 PRELIMINARY; PRT: 818 AA.
AC 091742;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FIBROBLAST GROWTH FACTOR RECEPTOR 4 PRECURSOR (FGFR-4) (EC 2.7.1.112).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95137391; PubMed=7835703;
RA Shiozaki C., Tashiro K., Asano-Miyoshi M., Saigo K., Emori Y.,
RA Shiozaki K.;
RT "Cloning of cDNA and genomic DNA encoding fibroblast growth factor
RT receptor-4 of Xenopus laevis."
RL Gene 152:215-219(1995).
CC -1- FUNCTION: RECEPTOR FOR ACIDIC FIBROBLAST GROWTH FACTOR. DOES NOT
CC BIND TO BASIC FIBROBLAST GROWTH FACTOR.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DEVELOPMENTAL STAGE: IT IS A MATERNAL PROTEIN WHICH DECREASES
CC GRADUALLY TO THE LATE BLASTULA STAGE AND THEN INCREASES BY ZYGOTIC
CC EXPRESSION REACHING A MAXIMUM AT THE BLASTULA AND THE LATE
CC GASTRULA STAGES.
CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR
CC FAMILY.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. THE
CC EXTRACELLULAR DOMAINS CONTAINS 3 IG-LIKE DOMAINS.
DR EMBL: D31761; BAA06539.1; -.
DR HSP; P06239; 3ICK.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00047; Ig; 3.
DR Pfam: PF00069; Pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00408; IGG2; 3.
DR SMART: SM00219; TYRKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50019; PROTEIN_KINASE_TYR; 1.
DR Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW Receptor; Glycoprotein; Tyrosine-protein kinase; Immunoglobulin domain;
KW Transferrase; Phosphorylation; Transmembrane; Immunoglobulin domain;
KW Signal.
FT CHAIN 1 26 POTENTIAL.
FT CHAIN 27 818 FGF RECEPTOR 4.
FT TRANSMEM 27 381 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 27 381 POTENTIAL.
FT DOMAIN 382 402 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 403 818 IG-LIKE DOMAIN.
FT DOMAIN 56 115 IG-LIKE DOMAIN.
FT DOMAIN 177 243 IG-LIKE DOMAIN.
FT DOMAIN 276 352 IG-LIKE DOMAIN.
FT DOMAIN 479 767 PROTEIN KINASE.
FT NP_BIND 485 493 ATP (BY SIMILARITY).
FT BINDING 515 515 ATP (BY SIMILARITY).
FT AC_SITE 624 624 BY SIMILARITY.
FT MOD_RES 655 655 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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Db 201 EHRIGYKVRNQHMSLIMESVPSDKNGYTCVENDYGSINH7YHLDVRSRPHRPILOA 260  
QY 249 THPVNTVDFGCTTSFOCKVRSVDKRPVIOMLKRE-----YGAEG-----RHNSTIDV 296  
Db 261 GLPNASTVVGDDVEFCVKYSDAOPHIOMIKHEKNGSKYGPDLPLYLKLKHSG---I 317  
QY 297 GGQKFEVLPETGVDWSRPGSYLNK 320  
Db 318 NSSNAEVLAFNVTEDAGEYICK 341  
RESULT 20  
012922  
ID 012922 PRELIMINARY; PRT; 366 AA.  
AC 012922;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE SOLUBLE KERATINOCYTE GROWTH FACTOR RECEPTOR PRECURSOR (BC 2.7.1.112).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BREAST, AND CORNEA.  
RX MEDLINE=95170769; PubMed=7866434;  
RA Wilson S.E., Weng J., Chwang E.L., Gollahon L., Leitch A.M.,  
RA Shay J.W.;  
RT "hepatocyte growth factor (HGF), keratinocyte growth factor (KGF), and  
RT their receptors in human breast cells and tissues: alternative  
RL Cell. Mol. Biol. Res. 40:337-350(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BREAST, AND CORNEA;  
RX MEDLINE=92108030; PubMed=1309608;  
RA Miki T., Bottaro D.P., Fleming T.P., Smith C.L., Burgess W.H.,  
RA Chan A.M., Aaronson S.A.;  
RT "Determination of ligand-binding specificity by alternative splicing:  
RT two distinct growth factor receptors encoded by a single gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:246-250(1992).  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
DR EMBL: U11814; AAA68514.1; -;  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00047; Ig; 3.  
DR SMART: SM00408; IGC2; 3.  
KW Receptor; Glycoprotein; Immunoglobulin domain; Signal; Keratin.  
FT SIGNAL 1 21  
FT CHAIN 22 366  
FT DOMAIN 55 114  
FT DOMAIN 172 238  
FT DOMAIN 271 349  
FT DISULFID 62 107  
FT DISULFID 179 231  
FT DISULFID 278 340  
FT CARBOHYD 83 123  
FT CARBOHYD 123 123  
FT CARBOHYD 228 228  
FT CARBOHYD 241 241  
FT CARBOHYD 265 265  
FT CARBOHYD 297 297  
FT CARBOHYD 318 318  
FT CARBOHYD 331 331  
SQ SEQUENCE 366 AA; 40614 MW; C02708836203465F CRC64;

QY 23 PPEAQRRTSRSHGRMPAGPHCAAVPEG-----DPEPLTMTKDGRTIHSGMSRF 75  
Db 35 PPEPRTKTOI-----SQPEVYVAAPGESLEVRCLLKDAVAISMTKDG--VHIGPNR 84  
QY 76 RVL-FOGLKVRKOVEREDAGVYCKATNGFSLSVNTVLVLLDDISPGKESLGPDSGSGQ 134  
Db 85 TVLIGEVLIQIKGATPRDSGLVACTASRTVDSFTWTFMNVNTDAISSGD---EDDTGGA 140  
QY 135 EDPASQ---QMARPREFTQPKMRRIYARPVGSSVRLKCVASGHPRPDITMKDQALT- 190  
Db 141 EDFVSESNNNKRAPYWTETKEKERRLHVAANTVVKFCPCAGNPMPTRMILKNKEFEQ 200  
QY 191 --RPAARPRKKKWTLSLKNLRPDSKGYTCVSRAGAINTYVDYQRTSRPVLTG 248  
Db 201 EHRIGYKVRNQHMSLIMESVPSDKNGYTCVENDYGSINH7YHLDVRSRPHRPILOA 260  
QY 249 THPVNTVDFGCTTSFOCKVRSVDKRPVIOMLKRE-----YGAEG-----RHNSTIDV 296  
Db 261 GLPNASTVVGDDVEFCVKYSDAOPHIOMIKHEKNGSKYGPDLPLYLKLKHSG---I 317  
QY 297 GGQKFEVLPETGVDWSRPGSYLNK 320  
Db 318 NSSNAEVLAFNVTEDAGEYICK 341  
RESULT 21  
090IH3  
ID 090IH3 PRELIMINARY; PRT; 768 AA.  
AC 090IH3;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE K-SAM-1103.  
DE K-SAM.  
GN K-SAM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H.,  
RA Ishii H., Yanagihara K., Mafune K., Makuchi M., Terada M.;  
RT "Deletion of the carboxyl-terminal exons of k-sam/FGFR2 by short  
RT homology-mediated recombination, generating preferential expression of  
RT specific mRNAs.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX  
DOMAIN.  
DR EMBL: AB030078; BAA89301.1; -;  
DR HSSP; P12931; IEK.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003598; Ig\_c2.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR001245; Tyr\_kin.  
DR Pfam; PF00047; Ig; 3.  
DR Pfam; PF00069; pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR SMART; SM00408; IGC2; 3.  
DR SMART; SM00219; TYRK; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Transferase; Tyrosine-protein kinase.  
SQ SEQUENCE 768 AA; 86208 MW; A6F1A35DD69FAPAAA CRC64;

Query Match 21.1%; Score 375.5; DB 4; Length 768;  
Best Local Similarity 29.9%; Pred. No. 4.4e-24;  
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;

QY 23 PPEAQRRTSRSHGRMPAGPHCAAVPEG-----DPEPLTMTKDGRTIHSGMSRF 75  
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;

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Db 35 PEEPPKTYOI-----SOPEVYVAAGSELEVERCLIKDAVISMWKDG--VHLGPNNR 84
QY 76 RVL-POGLKVKOVEREDAGVYVCKATNGFSLNVTLLVLDISPGEISGPDSSSGQ 134
Db 85 TVLIGETLIQKATPRDSGLACTASRTVDSFTWYFMVNTDAISSGD---EDDTDGA 140
QY 135 EDPASQ---OWARPRFTOPSMMRRRVIAIPVGS SVRLKCVASGHPRPDITMMDQALT- 190
Db 141 EDFESENSNNKRAPYWNTEKMERKRLHVAAPANTVFKRCAGGPNMPTMRLKNGKFERQ 200
QY 191 --REAAEPKKKWTLSLKNLRPEDSGKYTCRVSNRGAINATYKVDVIOFTNSKPYLTG 248
Db 201 EHRIGYKVRNQHMSLIMESVPSDKGNTCVVENEYGSINHYYHLDVERSPHRPILOA 260
QY 249 THPNTVTVDGCGTTSFQCKVRSVDKVPYIOMLKRYE-----YGAEG-----RHNSITDV 296
Db 261 GLPAMASTVVGDEVEFCCKYSDAQPHIOMIKHYEKNKSKYGPDLPLYLKLVHSG---I 317
QY 297 GGQKFEVVLPTGDVWSRPDGSYLK 320
Db 318 NSSNAEVLALFNVTADAGEYICK 341

RESULT 22
Q90IH5 PRELIMINARY; PRT; 771 AA.
AC Q90IH5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE K-SAM-1101.
GN K-SAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H.,
RA Ishii H., Yanagihara K., Matune K., Makuuchi M., Terada M.;
RT "Deletion of the carboxyl-terminal exons of K-sam/GGFR2 by short
RT homology-mediated recombination, generating preferential expression of
RT specific mRNAs.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AB030076; BAA89299.1; -.
DR HSSP; P12931; 1FMK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003598; Iq_C2.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR001245; Tyr_kin.
DR pfam; PF00047; Iq; 3.
DR pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00408; Igc2; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 771 AA; 86505 MW; BFC73746F1A35DD6 CRC64;
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Query Match 21.1%; Score 375.5; DB 4; Length 771;  
Best Local Similarity 29.9%; Pred. No. 4.4e-24;  
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;

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QY 23 PEPAPQRMKTRNSHGKWPAGPHCAAVPEG-----DPPILMTWKDGRTHSGWSRF 75
Db 35 PEEPPKTYOI-----SOPEVYVAAGSELEVERCLIKDAVISMWKDG--VHLGPNNR 84
QY 76 RVL-POGLKVKOVEREDAGVYVCKATNGFSLNVTLLVLDISPGEISGPDSSSGQ 134
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Db 85 TVLIGETLIQKATPRDSGLACTASRTVDSFTWYFMVNTDAISSGD---EDDTDGA 140
QY 135 EDPASQ---OWARPRFTOPSMMRRRVIAIPVGS SVRLKCVASGHPRPDITMMDQALT- 190
Db 141 EDFESENSNNKRAPYWNTEKMERKRLHVAAPANTVFKRCAGGPNMPTMRLKNGKFERQ 200
QY 191 --REAAEPKKKWTLSLKNLRPEDSGKYTCRVSNRGAINATYKVDVIOFTNSKPYLTG 248
Db 201 EHRIGYKVRNQHMSLIMESVPSDKGNTCVVENEYGSINHYYHLDVERSPHRPILOA 260
QY 249 THPNTVTVDGCGTTSFQCKVRSVDKVPYIOMLKRYE-----YGAEG-----RHNSITDV 296
Db 261 GLPAMASTVVGDEVEFCCKYSDAQPHIOMIKHYEKNKSKYGPDLPLYLKLVHSG---I 317
QY 297 GGQKFEVVLPTGDVWSRPDGSYLK 320
Db 318 NSSNAEVLALFNVTADAGEYICK 341
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RESULT 23
Q90IH4 PRELIMINARY; PRT; 817 AA.
AC Q90IH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE K-SAM-1102.
GN K-SAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H.,
RA Ishii H., Yanagihara K., Matune K., Makuuchi M., Terada M.;
RT "Deletion of the carboxyl-terminal exons of K-sam/GGFR2 by short
RT homology-mediated recombination, generating preferential expression of
RT specific mRNAs.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AB030077; BAA89300.1; -.
DR HSSP; P12931; 1FMK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003598; Iq_C2.
DR InterPro; IPR003006; Iq_MHC.
DR InterPro; IPR001245; Tyr_kin.
DR pfam; PF00047; Iq; 3.
DR pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00408; Igc2; 3.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 817 AA; 91718 MW; A84ED3EFBD0D1B77 CRC64;
```

Query Match 21.1%; Score 375.5; DB 4; Length 817;  
Best Local Similarity 29.9%; Pred. No. 4.7e-24;  
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;

```
QY 23 PEPAPQRMKTRNSHGKWPAGPHCAAVPEG-----DPPILMTWKDGRTHSGWSRF 75
Db 35 PEEPPKTYOI-----SOPEVYVAAGSELEVERCLIKDAVISMWKDG--VHLGPNNR 84
QY 76 RVL-POGLKVKOVEREDAGVYVCKATNGFSLNVTLLVLDISPGEISGPDSSSGQ 134
Db 85 TVLIGETLIQKATPRDSGLACTASRTVDSFTWYFMVNTDAISSGD---EDDTDGA 140
```

QY	191	--RPEA	PRKKKWTLS	KNLRPEDSGKYTC	CVNSRA	GAINATY	VVDYI	QI	TRSP	PVLTG	248	
Db	201	EHRI	GGYKVR	NOHMSL	IMESV	PSDKG	NTCT	VE	KEYS	INNTYH	DIVERSPHRPI	260
QY	249	THPV	TVTD	FGTTS	FOCK	RVSD	YV	PI	OW	LKRV	-----	296
Db	261	GI	PAAS	TVGG	DDVE	FKVY	SD	AP	PH	IO	IKV	296
QY	297	GG	KFV	LP	PTG	DW	SR	PD	GS	YLNK <td>320</td>	320	
Db	318	NSS	NEV	LA	LF	VT	TE	AD	AGE	YICK <td>341</td>	341	
RESULT	25											
Q9UIH7	09UIH7	PRELIMINARY;	PRT;	819	AA.							
AC	Q9UIH7:											
DT	01-MAY-2000	(TREMBLrel. 13, Created)										
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)										
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)										
DE	K-SAM-11H2	(FRAGMENT).										
GN	K-SAM.											
OS	Homo sapiens (Human).											
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;											
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.											
OX	NCBI_Taxid:9606;											
RN	[1]											
RP	SEQUENCE FROM N.A.											
RA	Ueda T., Sasaki H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H.,											
RA	Isih H., Yanagihara K., Maune K., Makuchi M., Terada M.;											
RT	"Deletion of the carboxyl-terminal exons of K-sam/FGFR2 by short											
RT	homology-mediated recombination, generating preferential expression of											
RT	specific mRNAs."											
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.											
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX											
CC	DOMAIN.											
DR	EMBL; AB030074; BAA89297.1; -.											
DR	HSSP; P12931; 1FWK.											
DR	InterPro; IPR000719; Euk.pkinase.											
DR	InterPro; IPR003598; Ig_c2.											
DR	InterPro; IPR003006; Ig_MHC.											
DR	InterPro; IPR001245; Tyr_kin.											
DR	Pfam; PF00047; Ig_3.											
DR	Pfam; PF00069; pkinase; 1.											
DR	PRINTS; PR00109; TYRKINASE.											
DR	SMART; SM00408; IGC2; 3.											
DR	SMART; SM00219; TYRK; 1.											
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.											
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.											
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.											
KW	ATP-binding; Transferase; Tyrosine-protein kinase.											
FT	NON_TER	819	819									
SO	SEQUENCE	819	AA;	91739	MM;	52D5955E7B76F4D9	CRC64;					
Query Match	21.1%;	Score	375.5;	DB	4;	Length	819;					
Best Local Similarity	29.9%;	Pred. No.	4.8e-24;									
Matches	97;	Conservative	55;	Mismatches	125;	Indels	43;	Gaps	10;			
QY	23	PEEA	QRM	TR	TR	SH	GR	MP	AG	PC	HA	296
Db	35	PEEP	TK	QI	-----	SQ	PE	VY	AA	AG	ES	296
QY	76	RVL	-PQ	LK	QV	ER	DA	GV	YV	CA	TG	296
Db	85	TVL	IG	EY	QI	QI	GA	MP	RD	SG	L	296
QY	135	EDP	AS	Q	-----	Q	A	R	P	F	Q	296
Db	141	EDP	Y	S	E	N	S	N	N	K	R	296
QY	191	--RPEA	PR	KK	K	W	T	L	S	K	N	248
Db	201	EHRI	GG	Y	K	V	R	N	O	H	M	260
QY	249	THPV	TV	T	D	F	G	T	T	S	F	296
Db	261	GI	PA	A	S	T	V	G	G	D	V	296
QY	297	GG	K	F	V	L	P	T	G	D	W	320
Db	318	NSS	N	E	V	L	A	L	F	V	T	341

```

Db      201 EHRIGGYKVNQHMSLIMESVPSDKGNTCVVENEYGSINHTYHLDVVERSPHPIQA 260
QY      249 THEVNTTVEGGETTSPOCKYRSDVKPYIQWLKRYE-----YGABG-----RHNSTIDY 296
Db      261 GLPANASTVVGDDVEVCVKYSDAPHIQWIKHVEKNKSKYGPDLPLYLKLKHSG--T 317
QY      297 GGOKFVLLPTGVDWSRPDGSYLNK 320
Db      318 NSSNAEVLALFNVTADAGEYICK 341

```

Search completed: May 2, 2002, 08:53:26  
 Job time: 202 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2002, 08:48:38 ; Search time 16.07 Seconds  
(without alignments)  
1526.335 Million cell updates/sec

Title: US-09-823-038A-33

Sequence: 1 RRA**PCC**CCSCCRRC**CG**PSHR.....VLPTGDVWSRPDGSYLNKPL 322

Scoring table: BLOSUM62

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : PIR\_68:✱

```
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	401	22.5	822	2	B49151	fibroblast growth
2	395	22.2	822	2	S19647	fibroblast growth
3	391.5	22.0	800	1	TVHD07	fibroblast growth
4	391	22.0	800	2	A48991	heparin-binding g
5	391	22.0	801	2	I55363	fibroblast growth
6	386	21.7	824	2	S24108	protein-lysozyme
7	384.5	21.6	822	2	B54846	fibroblast growth
8	384	21.6	797	2	S38579	fibroblast growth
9	382	21.5	823	2	B35963	fibroblast growth
10	381.5	21.4	812	1	A56477	protein-lysozyme
11	378	21.2	806	1	TVHD073	fibroblast growth
12	377	21.2	818	2	JC4058	fibroblast growth
13	375.5	21.1	769	2	S16236	fibroblast growth
14	375.5	21.1	806	2	A35963	protein-lysozyme
15	375.5	21.1	822	2	A45081	fibroblast growth
16	375.5	21.1	822	2	A41784	keratinocyte grow
17	374	21.0	825	2	UC4583	fibroblast growth
18	371.5	20.9	821	1	TVHD02	fibroblast growth
19	368.5	20.7	814	1	A39752	fibroblast growth
20	368.5	20.7	821	1	TVMSRK	fibroblast growth
21	364.5	20.5	822	2	I49289	fibroblast growth
22	363	20.4	480	2	A56182	fibroblast growth
23	362.5	20.4	822	2	TVHD04	fibroblast growth
24	362.5	20.3	822	2	S29840	fibroblast growth
25	362	20.3	480	2	B51892	fibroblast growth
26	362	20.3	832	2	JH0393	fibroblast growth
27	360.5	20.3	662	2	C40862	heparin-binding g
28	360.5	20.3	822	1	TVHD08	fibroblast growth
29	358.5	20.2	799	2	S18209	fibroblast growth

30	358.5	20.2	819	1	TYCH0020
31	356.5	20.0	861	2	PMO0302
32	356.5	20.0	824	2	S56439.9
33	355.5	20.0	820	2	S17235.5
34	354	19.9	816	2	AA9151.3
35	353.5	19.9	822	1	TYMS363.2
36	353.5	19.9	822	1	AA9151.3
37	354	18.2	353	2	S51242.2
38	318	17.9	682	2	AS5656.6
39	315	17.7	713	2	S150128
40	307	17.3	707	2	AS4844.6
41	307	17.3	707	2	AS4844.6
42	307	17.3	729	2	AS67950.5
43	305	17.1	733	2	TA9293.9
44	304	17.1	302	2	C26464.4
45	304	17.1	705	2	S516135.5
46	283.5	15.9	748	2	S41050.1
47	283.5	15.9	750	2	S41051.1
48	282	15.9	650	1	JC1455.1
49	257	14.4	254	2	CA2691.1
50	254	14.3	2029	1	TDFE131.1
51	243.5	13.7	790	2	AS9627.2
52	243.5	13.7	1052	2	BA9120.2
53	237	13.3	1612	2	T308085.0
54	234.5	13.2	483	2	T17346.9
55	233	13.1	423	2	T2954.9
56	233	13.1	1273	2	T42405.5
57	232.5	13.1	5175	2	T20992.2
58	232.5	13.1	5198	2	T43282.0
59	230.5	13.0	946	1	AA7299.9
60	230	12.9	1651	2	TA1416.0
61	226.5	12.7	4391	2	AS3257.9
62	225	12.6	1239	2	AS8096.6
63	224	12.5	3707	2	S18352.2
64	221.5	12.5	729	2	AA9120.2
65	220	12.4	1344	2	TA1431.0
66	218.5	12.3	6642	2	T29757.5
67	213.5	12.0	1256	2	T030976.6
68	210.5	11.8	1091	2	AS85823.2
69	209.5	11.8	1033	2	S19247.7
70	208	11.7	1040	2	AS7638.8
71	207	11.6	1103	2	T22869.9
72	207	11.6	1447	2	AS4100.0
73	206.5	11.6	6658	2	T13931.1
74	206	11.6	871	1	TA4869.6
75	206	11.6	881	1	TA4869.6
76	205.5	11.6	1427	1	TA1565.5
77	205	11.5	772	2	T13307.8
78	204	11.5	1240	2	T03097.7
79	204	11.5	1501	2	S15814.8
80	204	11.5	1863	2	S46171.7
81	203	11.4	1907	2	SS08933.3
82	203	11.4	1907	2	SS08933.3
83	202.5	11.4	1040	2	AS4695.5
84	202	11.4	1272	2	S26180.2
85	201.5	11.3	1499	2	T10212.2
86	201.5	11.3	1020	2	S05944.4
87	201.5	11.3	1912	2	AS6117.4
88	201.5	11.3	2541	2	T29340.0
89	201	11.3	2783	2	T43416.0
90	200	11.3	4162	2	T42633.3
91	200	11.2	1262	2	BA8758.8
92	200	11.2	1496	1	AA8758.8
93	199.5	11.2	1896	2	T08851.1
94	199	11.2	1277	2	T305322.2
95	199	11.2	1375	2	T138322.2
96	199	11.2	1526	2	T13833.3
97	198.5	11.2	1018	2	JC4211.1
98	198.5	11.2	1894	2	CS4689.9
99	197.5	11.0	1021	2	AS4774.2
100	196.5	11.0	1021	2	AS5711.2

## ALIGNMENTS

RESULT 1  
B49151  
fibroblast growth factor receptor 4 - Iberian ribbed newt  
C:Species: Pleurodeles walli1 (Iberian ribbed newt)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 16-Jul-1999  
C:Accession: B49151  
R:Shi, D.L.; Feige, J.J.; Riou, J.F.; Desimone, D.W.; Boucaut, J.C.  
Development 116, 261-273, 1992  
A:Title: Differential expression and regulation of two distinct fibroblast growth factors  
A:Reference number: A49151; MUID:93130775  
A:Accession: B49151  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-822 <SH2>  
A:Cross-references: GB:X65059; NID:g64252; PIDN:CMA46192.1; PID:g64253  
A:Experimental source: tail-bud  
A>Note: Sequence extracted from NCBI backbone (NCBIN:122598, NCBI.P:122599)  
C:Superfamily: basic fibroblast growth factor receptor 1; Immunoglobulin homology; prote  
C:Keywords: Arp; growth factor receptor  
F:283-354/Domain: immunoglobulin homology <IMM>  
F:484-769/Domain: protein kinase homology <KIN>  
F:492-500/Region: protein kinase ATP-binding motif

Query Match	22.5%	Score 401;	DB 2;	Length 822;
Best Local Similarity	32.8%	Pred. No. 5.9e-21;		
Matches	90;	Conservative	58;	Mismatches 106;
				Indels 20;
				Gaps 7;

```

QY      61  WTKGRTIHSQMSFFRYLPQGLKQKQYEREDAGVYVCATKGFSSLVNLTLYLDDISP 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      80  YTESTRLQHG- -RIRLDVLLEYLADVTYEDSGLYLC- -VPGCHILRNLTISVDSLAS 136

QY      121  G-- -KESIGPPSSSG--GQEDPASQOMARPREFTOPSKMRRRVITARPVSSSVRLKCVASGH 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      137  GDDDEDEHGRDSDGMDGEPPEYETSTRAPFWSOQPMDEKLLYAVPAGNYTFKCPISAGN 166

QY      176  PRPDITWAKDQOAL- - -TRPEAARPKKWTLSLKNLRPDESGYKTCRVSNRGAITATY 232
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      197  PTEGIRMLKNRREGGGEHRIGITLIRQIHNSLVNESVYPSDRGNYTLVLENKRGESISYST 256

QY      233  KVDYIQRTRSKSPVLTGTHPVNVTYDESGTTSFOCKVRSDVKPYVLIWLKRYE- - -YGAE 287
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      257  LLDVLEKSPHPRILIOALPLANTTEAMLGSDVOFECKVYSDAOPIHOLMKHIEVMSRRGPD 316

QY      288  G- - -RHNSTIDYGOKFEVYLPFGDWSRRDGSY 317
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      317  GVPEVOYLKTADINSSVEVLYLHNVSFEEDAGEY 350

```

RESULT 2  
S19947  
fibroblast growth factor receptor - Iberian ribbed newt  
C.Species: pleurodeles waltlil (Iberian ribbed newt)  
C.Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999  
C.Accession: S19947  
R.Shu, D.L.; Fejge, J.J.; Riou, J.F.; Desimone, D.W.; Boucaut, J.C.  
Submitted to the EMBL Data library, March 1992  
A.Description: Receptores during early development of the urodele Pleurodeles waltlil.  
A.Reference number: S19947  
A.Accession: S19947  
A.Status: preliminary  
A.Molecule type: mRNA  
A:Residues: 1-822 <SMT>  
A:Cross-references: EMBL:X65059  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; proteaf  
C:Keywords: Arp; growth factor receptor  
F:283-354/Domain: immunoglobulin homology <IMM>  
F:484-759/Domain: protein kinase homology <KIN>  
F:492-500/Region: protein kinase ATP-binding motif

Query Match	22.2%;	Score 395;	DB 2;	Length 822;
Best Local Similarity	32.5%;	Pred. No. 1.6e-20;		
Matches	89;	Conservative	58;	Mismatches 107;
			Indels	20;
			Gaps	7;

```

QY      61 WTKGRTTHSHSMSEFPVLPQJLCKYQYERADAGYVCATNGSGSLSVNTVLVLDDISP 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      80 YTESRLOHG- -RIRLIDVQELADVTYEDSGIYL- -VPGIGHILKRFITISYDLSL 136

QY      121 G--KESIGPPSSSG--GOEDPASQOMARRPFPQPSKMRRTYIARPVSSVRLKCVASGH 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      137 GDDDEDEHGRDSDGMDGEPPYSTYSTRAPFWSQOPOMRKKLVAAGVATYFERPSAEN 196

QY      176 PRPDTYWKDDQAL- - -TREAAEPKKKKWTLSLKNLRPEDSGKYCYCRNSNAGAINATY 232
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      197 PTPGRMLKNGREREGHRIIGIRLIRHQHSLIMESVYSDRKNYCIJLLENKFGSISYX 256

QY      233 KVDYIQIRKRPVLTGHPVNTTYVDGCGTTSFOCKYRSDVKPYIOMLKVE- - -YGAE 287
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      257 LLDVLESRPHRPIIOAGLIPANTYAMLGSDVQFCKYVSDAOPHIOMLKHEIYVNSRGYGD 316

QY      288 G- - -RHNSDTGCGKFVVLPTGDWMSRDEGY 317
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      317 GVPEVQVLKTDADINSSEVEVLVIHNNSEFDAGET 350

```

### RESULT 3

fibroblast growth factor receptor flg-2 precursor - human  
N:contants: protein-tyrosine kinase (EC 2.7.1.112) flg-2  
C:Species: Homo sapiens (man)  
C:Idate: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jun-2000  
C:Accession: A60350; S21843  
R:AY141, A.; Zimmer, Y.; Yayon, A.; Yarden, Y.; Givol, D.  
Oncogene 6, 1089-1092, 1991  
A:Title: Flg-2, a new member of the family of fibroblast growth factor receptors.  
Reference number: A60350. with A126260

A:Accession: A60350  
A:Molecule type: mRNA  
A:Residues: 1-800 <AVT>  
A:Cross-references: EMBL:Y58255; NID:g31382; PIDD:CAAA1209.1; PID:g31383  
A:Experimental source: keratinocytes  
C:Comment: This may be a receptor for keratinocyte growth factor.  
C:Genetics:  
A:Gene: GDB:R5FR2; JWS; C9D1; KGF; FLG2  
A:Cross-references: GDB:127273; OMIM:176943

C:Superfamily basic fibroblast growth factor receptor 1; immunoglobulin homology; pC:Keywords: ATP, autophosphorylation; duplication; glycoprotein; growth factor receptF:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-800/Product: fibroblast growth factor receptor lig-2 #status predicted <MAT>  
F:22-369/Domain: extracellular #status predicted <EXT>  
F:131-137/Region: acidic  
F:262-335/Domain: immunoglobulin homology <IMM>  
F:370-390/Domain: transmembrane #status predicted <TM>  
F:391-800/Domain: intracellular #status predicted <INT>  
F:464-749/Domain: protein kinase homology <KIN>  
F:472-480/Region: protein kinase ATP-binding motif  
F:59-107, 170-222, 269-333/Disulfide bonds: #status predicted  
F:96, 219, 256, 288, 309, 322/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:502, 519, 611/Active site: Lys, Glu, Asp #status predicted  
F:616, 629/Binding site: magnesium (Asn, Asp) #status predicted  
F:642/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match	22.08;	Score 391.5;	DB 1;	Length 800;
-------------	--------	--------------	-------	-------------

Best Local Similarity	31.9%;	Pred. No. 2.7e-20;
Matches	99; Conservative	49; Mismatches 129;
		Indels 33; Gaps 8

QY 5 CCCSCCRCCWPSHRPPPEAPQWRWTRMSHGRWAPGPHCAA-----AVPEEGD 54  
| : | | | : | |  
Db 6 CVLVFCVAVVAGATSEPPGPEQRRVVRRAAEVPGPEPSQEQVAFGSGDVELSCHPPGGA 65



R:Sato, M.; Kitazawa, T.; Iwai, T.; Seki, J.; Sakato, N.; Kato, J.; Takeya, T.  
Oncogene 6, 1279-1283, 1991  
A:Title: Isolation of chicken bck and a related gene; identification of structural varia  
A:Reference number: S24108; MUID:91319411  
A:Accession: S24108

A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-824 <SAT>  
A:Cross-references: EMBL:X61992; NID:963085; PIDN:CA043965.1; PID:963086  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: ATP; growth factor receptor; phosphotransferase; tyrosine-specific protein k  
F:174-235/Domain: immunoglobulin homology <IMM>  
F:482-767/Domain: protein kinase homology <KIN>  
F:490-498/Region: protein kinase ATP-binding motif

Query Match 21.7%; Score 386; DB 2; Length 824;  
Best Local Similarity 29.3%; Pred. No. 6.9e-20;  
Matches 97; Conservative 59; Mismatches 117; Indels 58; Gaps 11;

QY 23 PPEAPQRMWRMSHGRMPAGPHCAAVVEGDPPL-----TWTKG-----R 66  
DB 38 PPEPTKYQI-----SQPDVHSALP--GEPELKCQLKDAVMISWTKDGVPLGPDNR 87  
QY 67 THSGMSRFRVLPQGLKVKQVERDAGVYCKATNGFGLSVNTLVLDISPGEKSLG 126  
DB 88 TV-----IIGELYLIKDAISPRDSGLYACTAIRLDSPTLYIVNTALSSGDD--- 136  
QY 127 PDSSSGGQED--PASQOMAPRFTQPSKMRRIARVGVSSVRLKCVASGHPREDITWMLK 184  
DB 137 -EDNDSESDVDNSQMRAPYWHTKMEKRLHVAIPAANTVKEKPCAMGNPPTMRMLK 195  
QY 185 DDQALT--PPEAEPKRRKWTLSLKNLRPDSGKYTCRVSNRGAINATYKVDVIOCTR 241  
DB 196 NGKEFEQEHRIIGYKVKANQMSLIMESVPSDKNTICYENQGSINHTYHLDVERSP 255  
QY 242 SKPLVLTGHVNTVTDGGTTSFOCKRSDVKYIOMLKRYE-----YGAEG-----R 289  
DB 256 HRLPLQAGLPMASAVVGGVEFEKCYSDAOPHIQWIKHVERNGSKYDGLPYQLVK 315  
QY 290 HNSTIDVGQKFFVLPFGDWSRDPGSYLNK 320  
DB 316 HSG---INSSNAEVLTLTYNTDADAGEYICK 343

RESULT 7  
B54846  
fibroblast growth factor receptor b precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 16-Jul-1999  
C:Accession: B54846  
R:Atkagil, Y.; Shrivastav, S.; Miki, T.; Sakaguchi, K.  
J. Biol. Chem. 269, 23743-23749, 1994  
A:Title: Molecular cloning and expression of the acidic fibroblast growth factor recepto  
ility and covalent attachment of heparan sulfate glycosaminoglycan to the receptors.  
A:Reference number: A58466; MUID:94375464  
A:Accession: B54846  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-822 <TAK>  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: ATP; growth factor receptor  
F:172-233/Domain: immunoglobulin homology <IMM>  
F:480-765/Domain: protein kinase homology <KIN>  
F:488-496/Region: protein kinase ATP-binding motif

Query Match 21.6%; Score 384.5; DB 2; Length 822;  
Best Local Similarity 30.2%; Pred. No. 8.8e-20;  
Matches 97; Conservative 54; Mismatches 133; Indels 37; Gaps 9;  
QY 23 PPEAPQRMWRMSHGRMPAGPHCAAVVEG-----DPEPLTMTKDGRTTHSGMSR 75

DB 35 PPEPTKYQI-----SQPEACVAPAGSELRLCMKAOAIVSWTKDG--VHLGPNR 84  
QY 76 RVL--PQGLKVKQVERDAGVYCKATNGFGLSVNTLVLDISPGEKSLGPDSSGGQ 134  
DB 85 TVLIGELYLIKDAISPRDSGLYACTAIRLDSPTLYIVNTALSSGDD--- 144  
QY 135 EDPASQOMAPRFTQPSKMRRIARVGVSSVRLKCVASGHPREDITWMDQALT---R 191  
DB 145 SENNSNORA-PYMTNTEKMEKRLHVAIPAANTVKEKPCAMGNPPTMRMLKGEKQEH 203  
QY 192 PPEAEPKRRKWTLSLKNLRPDSGKYTCRVSNRGAINATYKVDVIOCTRSPVLTGTHP 251  
DB 204 IGGYKVARQMSLIMESVPSDKNTICYENQGSINHTYHLDVERSPHRLPQAGLP 263  
QY 252 VNTVTDGGTTSFOCKRSDVKYIOMLKRYE-----YGAEG-----RHNSTIDVGQ 299  
DB 264 AMASTVVGGVVEFYCKYSDAOPHIQWIKHVERNGSKYDGLPYLKLKHSQ---INSS 320  
QY 300 KFFVLPFGDWSRDPGSYLNK 320  
DB 321 NAEVLTALFNTDADAGEYICK 341

RESULT 8  
S38579  
fibroblast growth factor receptor 3 - Iberian ribbed newt (fragment)  
C:Species: Pleurodeles waltlil (Iberian ribbed newt)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 16-Jul-1999  
C:Accession: S38579  
R:Shi, D.L.; Fromentoux, V.; Launay, C.; Umbhaer, M.; Boucaut, J. C.  
submitted to the EMBL Data Library, November 1993  
A:Description: Expression of FGFR-3 in amphibian embryos.  
A:Reference number: S38579  
A:Accession: S38579  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-797 <SHI>  
A:Cross-references: EMBL:X75603  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; pr  
C:Keywords: ATP; growth factor receptor  
F:258-331/Domain: immunoglobulin homology <IMM>  
F:456-741/Domain: protein kinase homology <KIN>  
F:464-472/Region: protein kinase ATP-binding motif

Query Match 21.6%; Score 384; DB 2; Length 797;  
Best Local Similarity 33.8%; Pred. No. 9.2e-20;  
Matches 90; Conservative 41; Mismatches 87; Indels 48; Gaps 7;

QY 60 MMTKDGRTI-----HSGMSRFRVLPQGLKVKQVERDAGVYCKATNGFGLSVNTLV 113  
DB 67 VMKKGISVDPPTWSHTG-----QKLKIINVSVDGSGYSCKAROSSEYLR-NVYVR 118  
QY 114 VLDISPGEKSLGPDSSSGQEDPASQOMAPRFTQPSKMRRIARVGVSSVRLKCVAS 173  
DB 119 VTD-----SPSSGDEDEDESESANAPFTPEWMEKKILAVPANTVRFRCAPA 169  
QY 174 GHPRPDITWMDQALT---PPEAEPKRRKWTLSLKNLRPDSGKYTCRVSNRGAIA 230  
DB 170 GATPSTIWLKMKGEKGEHRIGIKLRHQQMSLVNESVPSDRGNTVAVANKYGTIRE 229  
QY 231 TYKVDVIOCTRSPVLTGTHPVNTVTDGGTTSFOCKRSDVKYIOMLKRYEYGAEGRH 290  
DB 230 TYLIDVLEHTPHRLPQAGFRSKTYVGSVDFEHCYVSDAOPHIQWLKRYE----- 282  
QY 291 NSTIDVGQKFFVLPFGDWSRDPGS 316  
DB 283 -----VNGSKF-----GPDGN 293

RESULT 9  
B35963  
protein-tyrosine kinase (EC 2.7.1.112) cek3 precursor - chicken

C:Species: Gallus gallus (chicken)  
C:Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 16-Jul-1999  
C:Accession: B35963  
R:Pasquale, E.B.  
A:Title: A distinctive family of embryonic protein-tyrosine kinase receptors.  
A:Reference number: A35963; MUID:90332672  
A:Accession: B35963  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-823 <PAS>  
A:Cross-references: GB:M35196; NID:g211444; PIDN:AAA48665.1; PID:g211445  
C:Genetics:  
A:Gene: cek3  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-823/Product: protein-tyrosine kinase cek3 #status predicted <MAT>  
F:23-379/Domain: extracellular #status predicted <EXT>  
F:135-141/Region: acidic  
F:174-235/Domain: immunoglobulin homology <IM>  
F:380-400/Domain: transmembrane #status predicted <TM>  
F:401-823/Domain: intracellular #status predicted <INT>  
F:489-497/Region: protein kinase ATP-binding motif  
F:65-110,181-233,280-344/Disulfide bonds: #status predicted  
F:220,267,299,320,333/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:519,536,628/Active site: Lys, Glu, Asp #status predicted  
F:633,646/Binding site: magnesium (Asn, Asp) #status predicted  
F:659/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 21.5%; Score 382; DB 2; Length 823;  
Best Local Similarity 30.8%; Pred. No. 1.3e-119;  
Matches 90; Conservative 54; Mismatches 10; Indels 48; Gaps 9;

QY 23 PPEAPQRMRTKMSHGRWAPGPHCAAVPEGDPPPL-----TWMTKG-----R 66  
DB 38 PEEPTTKYQI-----SQPDVHSALP--GEPLERQQLKDAWISWTKGCVLGPDPNR 87  
QY 67 TINSWMSFRVLPQGLVKQYERDAGVYVCATNGFSLSVNTLVLLDISPKESLG 126  
DB 88 TV-----IIGELYDIKIDASPRDSGLYACTAIRLTDSDTLVFLVNTALSSGDD--- 136  
QY 127 PDSSSGQED--PASQOMARPRFTQPSKMRVRVAPRGSSVRLKCAVSGHPRDITMK 184  
DB 137 -EDNDSEDEVDNSQMRAPYVHTDKMEKRLHAVPAANVTKPRCAMGNPTETMRWLK 195  
QY 185 DDOALT--RPEAEPKPKKWTLSLKNLRPDSGKYTCRVSNRAGATNATYKRVIOKTR 241  
DB 196 NGKEFKQDEHRIGKYKVRNQHMSTLMSVSPDKNYTCIVENQYGSINHTHTLHDVERS 255  
QY 242 SKPVLGTGHPVNTVDFGGTTSFOCKVRSVDKPYIOMLKRYE-----YGAGG 288  
DB 256 HRPILQAGLRANASAVVGGDVEFYCKVYSDAQPHIQWIKHNERGSKKGPBG 307

RESULT 10  
A36477  
fibroblast growth factor receptor A2 precursor - African clawed frog  
N:Contains: fibroblast growth factor receptor A2, short splice form, protein-tyrosine ki  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 08-Mar-1991 #sequence\_revision 19-Jan-1996 #text\_change 16-Jul-1999  
C:Accession: A36477; C39752  
R:Muscl, T.J.; Amaya, E.; Kirschner, M.W.  
Proc. Natl. Acad. Sci. U.S.A. 87, 8365-8369, 1990  
A:Title: Regulation of the fibroblast growth factor receptor in early Xenopus embryos.  
A:Reference number: A36477; MUID:91045998  
A:Accession: A36477  
A:Molecule type: mRNA  
A:Residues: 1-812 <MOS>  
A:Cross-references: GB:U24491; GB:M37201; NID:9857677; PIDN:AAA6868.1; PID:9857678  
A:Note: 45-Arg, 49-Thr, 50-Val, and 64-Ser also found

R:Frisesel, R.; David, I.B.  
Mol. Cell. Biol. 11, 2481-2488, 1991  
A:Title: cDNA cloning and developmental expression of fibroblast growth factor recept  
A:Reference number: A39752; MUID:91203867  
A:Accession: C39752  
A:Molecule type: mRNA  
A:Residues: 1-30,119-189,'G',191-418,'L',420-636,'R',638-788,'V',790-812 <FRI>  
A:Cross-references: GB:M62322; NID:g214899; PIDN:AAA4993.1; PID:g214900  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; pr  
C:Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein  
protein kinase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-812/Product: fibroblast growth factor receptor A2, long splice form #status pred  
F:22-372/Domain: extracellular #status predicted <EXT>  
F:22-30,119-812/Product: fibroblast growth factor receptor A2, short splice form #sta  
F:47-102/Domain: immunoglobulin homology <IM>  
F:125-132/Region: acidic  
F:167-228/Domain: immunoglobulin homology <IM2>  
F:266-339/Domain: transmembrane #status predicted <TM>  
F:373-393/Domain: immunoglobulin homology <IM3>  
F:394-812/Domain: intracellular #status predicted <INT>  
F:470-755/Domain: protein kinase homology <KIN>  
F:478-486/Region: protein kinase ATP-binding motif  
F:54-100,174-226,273-337/Disulfide bonds: #status predicted  
F:76,116,133,177,223,236,260,292,313,326/Binding site: carbohydrate (Asn) (covalent)  
F:508,525,617/Active site: Lys, Glu, Asp #status predicted  
F:622,635/Binding site: magnesium (Asn, Asp) #status predicted  
F:648/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

Query Match 21.4%; Score 381.5; DB 1; Length 812;  
Best Local Similarity 31.5%; Pred. No. 1.4e-19;  
Matches 95; Conservative 56; Mismatches 128; Indels 23; Gaps 10;

QY 20 RPP--PPEAPQRMRTKMSHGRWAPGPHCAAVPEGDPPPLTWMTKDGRTIHSGWSRFR 76  
DB 22 RPPSTLPDEVAPKRTKEVEPYSAQPGDRITLQCRLEDDVQGIN--VWKNQVLT--SETRNTR 79  
QY 77 VLPQGLAKKQYERDAGVYVCATNGFSLSVNTLV--VVLDISPKESLGPSSSG 133  
DB 80 ITGEIQLISNAGPDENGYAC-VYNG--PSRTYVLCISVNSDALPFAEDDEDDDDSS 135  
QY 134 QEDPASQOWA--RPFEPQSKMRVRVAPRGSSVRLKCVASGHPRPDITMKDDOALT 191  
DB 136 SEKRAAENSKRNRPLMSRPEKMEKKLHAVPAKYTKFCRPNAGPTPTPLRLKNNRAQO 195  
QY 192 PE---AAEPKPKKWTLSLKNLRPDSGKYTCRVSNRAGATNATYKRVYIOKTRSPVLTG 248  
DB 196 DQRIQGVVRSQVMSLIMDSVSPDKNYTCIVENKYGALNHQYQDIVERSPHRPILQA 255  
QY 249 THPVNTVDFGGTTSFOCKVRSVDKPYIOMLKRYEYGAEGRHNSITVDGQKRV-VLEPTG 307  
DB 256 GLPANTSVTGVTTAEFSCKVYSDQPHIQWIKHIEI-----NGSRVASDGPPEYELIKTA 310  
QY 308 DV 309  
DB 311 GV 312

RESULT 11  
TVHUP3  
fibroblast growth factor receptor 3 precursor - human  
N:Contains: protein-tyrosine kinase (BC 2.7.1.112)  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 16-Jul-1999  
C:Accession: A38576; A55273; E38269; I51880  
R:Keegan, K.; Johnson, D.E.; Williams, L.T.; Hayman, M.J.  
Proc. Natl. Acad. Sci. U.S.A. 88, 1095-1099, 1991  
A:Title: Isolation of an additional member of the fibroblast growth factor receptor f  
A:Reference number: A38576; MUID:91142118  
A:Accession: A38576  
A:Molecule type: mRNA  
A:Residues: 1-806 <KEE>

A:Cross-references: GB:M56051; NID:q182568; PIDN:AA52450.1; PID:q182569  
R:Thompson, L.M.; Plummer, S.; Schalling, M.; Altherr, M.R.; Gusella, J.F.; Housman, D.I.  
Genomics 11, 1133-1142, 1991  
A>Title: A gene encoding a fibroblast growth factor receptor isolated from the Huntington  
A:Reference number: A55273; MUID:92147110  
A:Accession: A55273  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 76-394, 'V', 396-806 <THO>  
A:Cross-references: GB:M64347; NID:q182564; PIDN:AA548470.1; PID:q182565  
A>Note: sequence extracted from NCBI backbone (NCBI:80296)  
R:Parfaneau, J.; Maekelaie, T.P.; Altitalo, R.; Lemhassalho, H.; Altitalo, K.  
Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990  
A>Title: Putative tyrosine kinases expressed in K-562 human leukemia cells.  
A:Reference number: A58268; MUID:91062389  
A:Accession: E38269  
A:Molecule type: mRNA  
A:Residues: 619-675 <PAR>  
A:Cross-references: GB:M37782  
R:Bellus, G.A.; Hefner, T.W.; Ortiz de Luna, R.I.; Hecht, J.T.; Horton, W.A.; Machado,  
M. J. Hum. Genet. 56, 368-373, 1995  
A>Title: Achondroplasia is defined by recurrent G380R mutations of FGFR3.  
A:Reference number: I51880; MUID:95150025  
A:Accession: I51880  
A>Status: translated from GR/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 361-379, 'R', 381-415 <RES>  
A:Cross-references: GB:S76733; NID:q914201; PIDN:AA833323.1; PID:q914202  
A>Note: this sequence represents a mutant form associated with achondroplasia  
C:Genetics:  
A:Gene: GDB:FGFR3  
A:Cross-references: GDB:127526; OMIM:100800; OMIM:134934  
A:Map position: 4p16.3-4p16.3  
C:Function:  
A:Description: receptor for both acidic and basic fibroblast growth factors  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-806/Product: fibroblast growth factor receptor 3 #status predicted <MAT>  
F:23-375/Domain: extracellular #status predicted <EXT>  
F:133-139/Region: acidic  
F:268-341/Domain: immunoglobulin homology <IMM>  
F:376-396/Domain: transmembrane #status predicted <TMN>  
F:397-806/Domain: intracellular #status predicted <INT>  
F:470-755/Domain: protein kinase homology <KIN>  
F:478-486/Region: protein kinase ATP-binding motif  
F:61-109, 116-228, 275-329/Disulfide bonds: #status predicted  
F:98-228, 262-294, 315-338/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:508-525, 617/Active site: Lys, Glu, Asp #status predicted  
F:622, 635/Binding site: magnesium (Asn, Asp) #status predicted  
F:648/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

	Query Match	Similarity	21.2%	Score 376	DB 1	Length 806
	Best Local	Similarity	31.8%	Pred. No. 2.5e-19		
	Matches	96	Conservative	54	Mismatches 118	Indels 34
					Gaps	10
QY	16	GPSHRRPPEAFQRMWTRMSHGFMWPA	PHCAAVPVEGDP--PL--TWMTKDGRTIHS	70		
		I I I I I I I I I I I I I I I I I I	I I I I I I I I I I I I I I I I I I			
Db	33	GAAAEVPEGEPEQOEQLVFGSG-----	DAVELSCPPGGSGPMPTVWVKGTGLVP	83		
QY	71	GMSRRFVLPQGLKVKQVEEDAGVYVC--	KATNGFGSLNVTILVYLDIDISPGKESLCPD	128		
		I I I I I I I I I I I I I I I I I I	I I I I I I I I I I I I I I I I I I			
Db	84	S-ERVLVGFQRLQVLNASHEDSGAYSC	RQRLTID--RVLCIFSVRYVDAPSSGDDEGED	139		
QY	129	SSSGQOEDPASQOMARPRFTOPSKMRR	RYIARVSGSVRLKCAVSGHPREDITMMKDOA	188		
		I I I I I I I I I I I I I I I I I I	I I I I I I I I I I I I I I I I I I			
Db	140	EAEDTGVDTGAAEYW-----	TRPERMDKILLVAPAMTVRRRCACAGNPTLS	194		
QY	189	LT-----RPEAEFRKKKKWTSLIKNL	RPEDSGKTYICRYSNRGAINATYKVDVIQTRSKPV	245		
		I I I I I I I I I I I I I I I I I I	I I I I I I I I I I I I I I I I I I			
Db	195	FRGHRIGIGIKIRHOOOSLVMSVESPS	DGNGYTCVVENKGSITROTTLVLLEKSSPRPI	254		

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QY      246  LTGTPVTWVDEGGTTSFOCKVRSDYKPVITQMLKRYEYGAEGRHNTPIDVGQKEV-VL 304
      255  LQAGPFAHQTVLGSVDVEFHCKYVSDAQPHIQMLKHVEV-----NGSKVGPDGPIPVTL 309
QY      305  PT 306
Db      310  KT 311

```

RESULT 12  
JC4058  
fibroblast growth factor receptor-4 precursor - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 29-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 20-Jun-2000  
C:Accession: JC4058  
R:Shiozaki, C.; Tashiro, K.; Asano-Miyoshi, M.; Salgo, K.; Emori, Y.; Shikawa, K.  
Gene 152, 215-219, 1995  
A:Title: Cloning of cDNA and genomic DNA encoding fibroblast growth factor receptor-4  
A:Reference number: JC4058; MUID:95137391

A: Molecule type mRNA  
A: Residues: 1-818 <SHIT>  
A: Cross-references: DDBJ:D31761; NID:g809527; PID:BAA06539.1; PID:g809528  
C: Genetics:  
C: Introns: 43/1; 125/1; 158/1; 213/1; 254/1; 318/1; 364/1; 429/1; 478/1; 556/1; 619/1  
C: Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein  
C: Keywords: ATP; growth factor receptor; transmembrane protein  
F: 1-26/Domain: signal sequence #status predicted <SIG>  
F: 27-818/Product: fibroblast growth factor receptor-4 #status predicted <MAT>  
F: 56-110/Domain: immunoglobulin homology <IM1>  
F: 133-137/Domain: acidic #status predicted <AD1>  
F: 177-238/Domain: immunoglobulin homology <IM2>  
F: 276-347/Domain: immunoglobulin homology <IM3>  
F: 382-402/Domain: transmembrane #status predicted <TM1>  
F: 477-762/Domain: protein kinase homology <KIN>  
F: 485-493/Region: protein kinase ATP-binding motif

[illegible]

```
RESULT 13
S16236
fibroblast growth factor receptor precursor - human
N:Alternate names: bck-related FGF receptor
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Jul-1999
C:Accession: S16236
R:Seno, M.; Sasada, R.; Watanabe, T.; Ishimaru, K.;
Itochim, M.; Biophys. Acta 1089, 244-246, 1991
Igarashi, K.
```









fibroblast growth factor receptor 2 precursor - human  
N:Alternate names: fibroblast growth factor receptor K-sam  
N:Contains: protein-tyrosine kinase (EC 2.7.1.112) bek; receptor-like protein-tyrosine k  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence\_revision 19-Jan-1996 #text\_change 16-Jul-1999  
C:Accession: A42691; B42691; S11691; A36210; B44775; D44775  
R:Kachoh, M.; Hattori, Y.; Sasaki, H.; Tanaka, M.; Sugano, K.; Yazaki, Y.; Sugimura, T.;  
Proc. Natl. Acad. Sci. U.S.A. 89, 2960-2964, 1992  
A:Title: K-sam gene encodes secreted as well as transmembrane receptor tyrosine kinase.  
A:Reference number: A42691; MUID:92212948  
A:Accession: A42691  
A:Molecule type: mRNA  
A:Residues: 1-821 <KAT>  
A:Cross-references: GB:M87770; NID:g186779; PIDN:AAA59470.1; PID:g186780  
A:Accession: B42691  
A:Molecule type: mRNA  
A:Residues: 1-313,430-821 <KA2>  
A:Cross-references: GB:M87771; NID:g186781; PIDN:AAA59471.1; PID:g186782  
R:Dione, C.A.; Crumley, G.; Bellot, F.; Kaplow, J.M.; Searfoss, G.; Ruta, M.; Burgess,  
EMBO J. 9, 2685-2692, 1990  
A:Title: Cloning and expression of two distinct high-affinity receptors cross-reacting w  
A:Reference number: S11691; MUID:90360977  
A:Accession: S11691  
A:Molecule type: mRNA  
A:Residues: 1-821 <DIO>  
A:Cross-references: EMBL:X52832; NID:g31373; PIDN:CAA37014.1; PID:g31374  
R:Housaint, E.; Blauquet, P.R.; Champion-Arnaud, P.; Gesnel, M.C.; Torriglia, A.; Court  
Proc. Natl. Acad. Sci. U.S.A. 87, 8180-8184, 1990  
A:Title: Related fibroblast growth factor receptor genes exist in the human genome.  
A:Reference number: A36210; MUID:91045961  
A:Accession: A36210  
A:Molecule type: mRNA  
A:Residues: 1-313, 'VUK', 314-428, 431-821 <HOU>  
A:Cross-references: GB:M55614; GB:M37715; NID:g339710; PIDN:AAA61188.1; PID:g339711  
R:Champion-Arnaud, P.; Ronshin, C.; Gilbert, E.; Gesnel, M.C.; Housaint, E.; Breathnach,  
Oncogene 6, 979-987, 1991  
A:Title: Multiple mRNAs code for proteins related to the BEK fibroblast growth factor re  
A:Reference number: A44775; MUID:91296403  
A:Accession: B44775  
A:Molecule type: DNA  
A:Residues: 263-361 <CH2>  
A:Cross-references: GB:S40858; NID:g232799; PIDN:AAB19320.1; PID:g232800  
A:Accession: D44775  
A:Molecule type: DNA  
A:Residues: 759-821 <CHA>  
A:Cross-references: GB:S41873  
C:Comment: This receptor binds basic fibroblast growth factor and, with lower affinity,  
C:Genetics:  
A:Gene: GDB:FGFR2  
A:Cross-references: GDB:127273; OMIM:176943  
A:Map position: 10q25.3-10q26  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote  
C:Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; g  
protein kinase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-821/Product: fibroblast growth factor receptor 2 #status predicted <MAT>  
F:132-377/Domain: extracellular #status predicted <EXT>  
F:132-136/Region: acidic  
F:172-398/Domain: immunoglobulin homology <IMM>  
F:378-398/Domain: transmembrane #status predicted <TM>  
F:399-821/Domain: intracellular #status predicted <INT>  
F:479-764/Domain: protein kinase homology <KIN>  
F:487-495/Region: protein kinase ATP-binding motif  
F:62-107,179-231,278-342/Dissulfide bonds: #status predicted  
F:83,123,228,241,265,297,318,331/Binding site: carbohydrate (Asn) (covalent) #status pre  
F:517,533,626/Active site: Lys, Glu, Asp #status predicted  
F:631,644/Binding site: magnesium (Asn, Asp) #status predicted  
F:657/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match 20.9%; Score 371.5; DB 1; Length 821;  
Best Local Similarity 31.6%; Pred. No. 7.3e-19;  
Matches 90; Conservative 50; Mismatches 112; Indels 33; Gaps 8;

23 PPEAPQRMWRMSHGKWPAGPCHCAAVPEG-----DPEPLTWTKDGRTHSGMSRF 75  
| | : : : : : | | | | | : : : : :  
Db PPEPPTKTYI-----SQPEVYVAAPGESLEVRCLKDAVAISWTKG--VHLSPNRR 84  
76 RVL-POGLVKOVERADGVYCAKATNGSLSVNVTVLVLDISPKESLGPDSSSGQ 134  
| | : : : : : | | | | | : : : : :  
Db TVLIGVLDIKATPRDSLTACTASRTYDSETFWVNTDAISSGD-----EDDTDA 140  
135 EDPASQ--QMARPRETPDSKMRRYIARPVSSVRLKCVASGHPRPDITMKDQALF- 190  
| | : : : : : | | | | | : : : : :  
Db EDVSESNKRPAPYWTNETKMEKRLHAVPAANTVFCRCPAGNPMPTRMLKNGKRFQ 200  
141  
191 --RPEAERKKKWTLSKLPEDSGKTCVSNRAGINATKYKVDQRRSKPVLTG 248  
| | : : : : : | | | | | : : : : :  
Db EHRIGGVKRVNDHWSLIMSEVSPDKGNTCVENEGSINTYHLIDVERSPHPILOA 260  
249 THPVNTVDFEGGTSFQCVRSQVDPVQIWKRV-----YGAEG 288  
| | : : : : : | | | | | : : : : :  
Db GIPANSTVVGQDVERCVKDYSDAQPHIOMIKHVENKSKYCPDG 305  
261

RESULT 19  
A39752  
fibroblast growth factor receptor A1 precursor - African clawed frog  
N:Contains: fibroblast growth factor receptor A1, short splice form; protein-tyrosine  
C:Species: Xenopus laevis (African clawed frog)  
C:Date: 07-Feb-1992 #sequence\_revision 19-Jan-1996 #text\_change 16-Jul-1999  
C:Accession: A39752; B39752  
R:Frlesel, R.; Dawid, I.B.  
Mol. Cell. Biol. 11, 2481-2488, 1991  
A:Title: cDNA cloning and developmental expression of fibroblast growth factor recept  
A:Reference number: A39752; MUID:91203867  
A:Accession: A39752  
A:Molecule type: mRNA  
A:Residues: 1-814 <FR1>  
A:Cross-references: GB:M55163; NID:g214893; PIDN:AAA49990.1; PID:g214894  
A:Accession: B39752  
A:Molecule type: mRNA  
A:Residues: 1-30,119-814 <FR2>  
A:Cross-references: GB:M55163  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; pr  
C:Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein  
protein kinase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-814/Product: fibroblast growth factor receptor A1, long splice form #status expe  
F:22-372/Domain: extracellular #status predicted <EXT>  
F:22-30,119-814/Product: fibroblast growth factor receptor A1, short splice form #sta  
F:47-102/Domain: immunoglobulin homology <IM1>  
F:125-133/Region: acidic  
F:167-228/Domain: immunoglobulin homology <IM2>  
F:266-333/Domain: transmembrane #status predicted <TM>  
F:373-393/Domain: intracellular #status predicted <INT>  
F:394-814/Domain: intracellular #status predicted <INT>  
F:472-757/Domain: protein kinase homology <KIN>  
F:480-488/Region: protein kinase ATP-binding motif  
F:54-100,174-226,273-337/Dissulfide bonds: #status predicted  
F:76,116,133,177,223,336,260,292,313,336/Binding site: carbohydrate (Asn) (covalent)  
F:510,527,619/Active site: Lys, Glu, Asp #status predicted  
F:624,637/Binding site: magnesium (Asn, Asp) #status predicted  
F:650/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi

Query Match 20.7%; Score 368.5; DB 1; Length 814;  
Best Local Similarity 29.7%; Pred. No. 1.2e-18;  
Matches 92; Conservative 57; Mismatches 122; Indels 39; Gaps 11;

20 RPP---PPEAPQRMWRMSHGKWPAGPCHCAAVPVGDPPL-----TMTTKDGR 66  
| | | | : : : : : | | | | | : : : : :  
Db 22 RPPSTLPDEVAARKTYE-----VEPYSAR---PGDVTTLQCRLEDVQGISWVKNKV 70  
67 THSGMSRFRVLPQGLKVKOVERADGVYCAKATNGSLSVNVTVLVLDISPKESLSG 126  
: | | : : : : : | | | | | : : : : : | | |

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Db 71 QLE-TNRRTIGETRIQISNAGPENGILYACTIGPSGTYVLFISIN-SDAPSAEDD 128
Oy 127 PDSSGGGDDPAAQOQA--RPRFTQPSKMRRIYARVPYSSRLKCAVSGHPRDITM 184
Db 129 DDDNSSEKASSENSKRRPFWSHPEKMEKLIHAVPAKTVKFCPCANGPSPALRMWK 188
Oy 185 DDQALTRPE---AAEPRKKWTLSLKNLRPDSGKYTCRVSNRGAINATYKVIVORT 240
Db 189 NGKEF-RPDQIRIGYKVASQTMVSLIMDSVPSDKGNITCYENKKYGTILNHTYQLDV 247
Oy 241 RSKPVLGTHVNTYVDGCGTTSPOCKVRSYKVPYIOWLKREYGAESRHNSTDVSGC 300
Db 248 PRRPLTQGLPANTSVTVGTAESFCYSDQPHIOWLMRIEIT-----NGSRVASDGF 302
Oy 301 FV-VLPRTGDV 309
Db 303 YVEILKTAGV 312

RESULT 20
fibrinblast growth factor receptor bek precursor - mouse
N:Alternate names: bek transforming protein; fibrinblast growth factor receptor 2; keratin
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1991 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
R:Musukhani, A.; Dell'Era, P.; Moscattelli, D.; Kornbluth, S.; Hanafusa, H.; Basilico, C.
P:Proc. Natl. Acad. Sci. U.S.A. 89, 3305-3309, 1992
A:Title: Characterization of the murine BEK fibrinblast growth factor (FGF) receptor: act
A:Reference number: A44142; MUID:92228773
A:Accession: A44142
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-821 <MAN>
A:Cross-references: GB:M86441
R:Kornbluth, S.; Paulson, K.E.; Hanafusa, H.
Mol. Cell. Biol. 8, 5541-5544, 1988
A:Title: Novel tyrosine kinase identified by phosphotyrosine antibody screening of cDNA
A:Reference number: A31378; MUID:89219016
A:Accession: A31378
A:Molecule type: mRNA
A:Residues: 477-821 <KOR>
A:Cross-references: GB:M23362; NID:9533219; PIDN:AAA37285.1; PID:9533220
A:Gene: bek
C:Genetics:
C:Superfamily: basic fibrinblast growth factor receptor 1; immunoglobulin homology; prote
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor;
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-821/Product: immunoglobulin growth factor receptor bek #status predicted <MAT>
F:112-233/Domain: immunoglobulin homology <IMM>
F:378-398/Domain: transmembrane #status predicted <TM>
F:479-764/Domain: protein kinase homology <KIN>
F:487-495/Region: protein kinase ATP-binding motif
F:62-107-179-231-278-342/Disulfide bonds: #status predicted
F:83,123,147,241,265,297,318,331/Binding site: carbohydrate (Asn) (covalent) #status pre
F:517,534,626/Active site: Lys, Glu, Asp #status predicted
F:557/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicte

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Db 145 SENSNORA-PYWTTEKMEKRLHACPAANTVTRCPGNGPSTMTMLKNGKEEKOHR 203
Oy 192 PEAAEPRKKKWTLSLKNLRPDSGKYTCRVSNRGAINATYKVIVORTSKPVLGTGP 251
Db 204 IGGYKVRNQHWSLIMESVPSDKGNITCYENKYSINHTYHLDVVERSPRRPLTQGLP 263
Oy 252 VNTYVDGCGTTSPOCKVRSYKVPYIOWLKRE-----YGAAG 288
Db 264 AMASTVGGDVEFYCKYSDAQPHIOWLKREKNGSKYGPDG 305

RESULT 21
fibrinblast growth factor receptor-1, long isoform precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
A:Accession: I49289
R:Jin, Y.; Pasumartli, K.B.; Bock, M.E.; Lytras, A.; Kardami, E.; Cattini, P.A.
J. Mol. Cell. Cardiol. 26, 1449-1459, 1994
A:Title: Cloning and expression of fibrinblast growth factor receptor-1 isoforms in th
A:Reference number: I49289; MUID:95205422
A:Accession: I49289
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-822 <RES>
A:Cross-references: EMBL:U022324; NID:g7223240; PIDN:MAC52182.1; PID:g722341
C:Superfamily: basic fibrinblast growth factor receptor 1; immunoglobulin homology; pr
C:Keywords: ATP; growth factor receptor
F:270-343/Domain: immunoglobulin homology <IMM>
F:476-761/Domain: protein kinase homology <KIN>
F:484-492/Region: protein kinase ATP-binding motif

```

```

Query Match 20.5%; Score 364.5; DB 2; Length 822;
Best Local Similarity 30.6%; Pred. No. 1.2e-18;
Matches 90; Conservative 47; Mismatches 106; Indels 51; Gaps 10;

Oy 20 RPPF--PEAQRRRTMSHGRWAGPCAAAYVE-----GDPPPLTM----- 60
Db 22 RPAFTLPDQAPW-----GVEVEESILVHPGDLLOLCRLRDVOST 64
Oy 61 -WTKDG-RTIHSGSRFRVLPQGLKRVQREDEAGYVVCATNGFSLSVNTYLVLDI 118
Db 65 NWLRDGYQVLES--NRRRTIGEEVAVDSIPADSGLYACTYSSPSGS-DITYSVANSDA 121
Oy 119 SPKESIGPPSSGGQEDPA-----SQQWARRPFTQPSKMRRIYARVPYSSVRLKCVAS 173
Db 122 LPSEDDDDDDSSSEKETDNTKPNRRPYAPVWTSPEKMEKLIHAVPAKTVKFCPPSS 181
Oy 174 GHRPRTMWMKDQALTRPE---AAEPRKKWTLSLKNLRPDSGKYTCRVSNRGAIN 229
Db 182 GTRNPFLRWLNKKEF-KPDHRTIGYKVRATATSTIMDSVPSDKGNITCYENEGSIN 240
Oy 230 ATYKVDVORTSKRPVLTGTHPVNTYVDGCGTTSPOCKVRSYKVPYIOWLKRE 283
Db 241 HTYQLDVVERSPRRPLTQGLPANEVYALGNSNVEFMCKYSDQPHIOWLKRIE 294

RESULT 22
A56182
fibrinblast growth factor receptor 2 isoform IIIB - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 19-Oct-1995 #sequence_revision 19-Jan-1996 #text_change 16-Jul-1999
A:Accession: A56182
R:Mathieu, M.; Kieffer, P.; Mason, I.; Dickson, C.
J. Biol. Chem. 270, 6779-6787, 1995
A:Title: Fibrinblast growth factor (FGF) 3 from Xenopus laevis (XFGF3) binds with high
A:Reference number: A56182; MUID:95204476
A:Accession: A56182
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-480 <MAT>

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C:Superfamily basic fibroblast growth factor receptor 1; immunoglobulin homology; protease  
C:Keywords: growth factor receptor  
E:183-244/Domain: immunoglobulin homology <IMM>

Query Match	20.4%;	Score 363;	DB 2;	Length 480;
Best Local Similarity	28.6%;	Pred. No. 1.6e-18;		
Matches	95;	Conservative	53;	Mismatches 120;
			Indels	64;
			Gaps	11;

Qy	21	PPPPAPRPMRTWMSHGWPAGPHCAAPV--EGEP-----PRTMTTKGRTHS	70
Db	49	PEPEPAPKYYQ-----SKADYFVLVGPEDLDRCPDLADGPLVYTWTKGAKLEY	97
Qy	71	GMSRFVLPGLKAYQVERDAGYVYCKATNGFSGLSVNTLVLLDDISPEKESIGDSS	130
Db	98	N-NRFLVIRTLQIKESTPRDSCGLYACSVLKNSHFFHNVV-----EASS	141
Qy	131	SGGQED--PASOAMR-----PRETPQSKRRVRVIRPVGSSVRLKCVASGHPRPIT	181
Db	142	SGDEDDDDSGEDFTNDNNNIRAPYWTETEKMEKKLHAPVPAANTYKLCRCPAGNPTPMR	201
Qy	182	WMKDDQALT---RPEAAEPKKKWTLSLKNLRPEDSGYTCRVSNRGAIAATYKVDYIQ	238
Db	202	WLKNKEKKEKQEHRIQGYVVRQOHMSLIMESVAPSPDKGYITCIVENEHSGSINHYYHLDYE	261
Qy	239	RTSRSPVLTGTHPVNTYVDFCGTTSFOCKVRSDVYVLOWLKRVE-----YGAEG-----	288
Db	262	RSSHHPILIOAGLPLANTIAVVGDAEFYCKVYSDAQPHIRWRYIIFKNGSRGVDGLPIYK	321
Qy	289	--RHNSTIDVGQKFVLLPTGDWMSRPDGYL	318
Db	322	VLKHSG---INSSSAEVLKLYNVTEADAGEYI	350

RESULT 23

TVHDF4  
fibroblast growth factor receptor 4 precursor - human

N:Alternate names: protein-tyrosine kinase tkf

N:Contains: protein-tyrosine kinase (EC 2.7.1.112)

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1993 #sequence,revision 31-Dec-1993 #text-change 16-Jul-1999

C:Accession: S15345; A46615; A41596; D38269

R:Patlanen, J.; Mekeläe, T.P.; Eerola, E.; Korhonen, J.; Hirvonen, H.; Claesson-Welsh, EMBL J. 10, 1347-1354, 1991

A:Title: FGFR-4, a novel acidic fibroblast growth factor receptor with a distinct expression pattern

A:Reference number: S15345; MUID:91224085

A:Accession: S15345

A:Molecule type: mRNA

A:Residues: 1-802 <PAR>

A:Cross-references: EMBL:X57205; NID:G91371; PID:CAA0490.1; PID:G91372

A:Note: binds acidic but not basic fibroblast growth factor with high affinity

R:Ron, D.; Reich, R.; Chedid, M.; Lengel, C.; Cohen, O.E.; Chan, A.M.; Neufeld, G.; Miki, J. Biol. Chem. 266, 5388-5394, 1993

A:Title: Fibroblast growth factor receptor 4 is a high affinity receptor for both acidic and basic fibroblast growth factors

A:Reference number: A46615; MUID:93194827

A:Accession: A46615

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-296,'D', 298-802 <RON>

A:Experimental source: mammary epithelial cell line B5/589

A:Note: sequence extracted from NCBI backbone (NCBI:127650)

A:Note: binds acidic and basic fibroblast growth factors with high affinity

R:Holtkamp, U.; Braennlinger, A.; Strebhardt, K.; Ruesamen-Welgmann, H. Proc. Natl. Acad. Sci. U.S.A. 88, 10411-10415, 1991

A:Title: Two additional protein-tyrosine kinases expressed in human lung: fourth member of the src family

A:Reference number: S19025; MUID:92073297

A:Accession: A41598

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 399-534,'W', 536-799,'SG', 800-802 <HOL>

A:Experimental source: lung

R:Patlanen, J.; Mekeläe, T.P.; Alltalo, R.; Lehtvaeslahti, H.; Alltalo, K. Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990

A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells  
A;Reference number: A38268; MUID:91062389

A:Accession: D38269  
A:Molecule type: mRNA  
A:Residues: 614-670 <PA2>  
A:Cross-references: GB:M57781  
A:Experimental source: K-562 leukemia cell line  
C:Genetics:  
A:Gene: GDB:FGFR4  
A:Cross-references: GDB:127929; OMTM:134935  
A:Map position: 5q33.2-5qter  
C:Function:  
A:Description: receptor mediating effects of fibroblast growth factor  
A:Note: expressed in normal lung; expressed in some carcinomas  
C:Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein tyrosine kinase  
C:Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor  
F:1-44/Domain: signal sequence #status predicted <SIG>  
F:125-802/Product: fibroblast growth factor receptor 4 #status predicted <MAT>  
F:125-369/Domain: extracellular #status predicted <EXT>  
F:50-103/Domain: immunoglobulin homology <IM1>  
F:165-226/Domain: immunoglobulin homology <IM2>  
F:264-335/Domain: immunoglobulin homology <IM3>  
F:370-390/Domain: transmembrane #status predicted <TM>  
F:391-802/Domain: intracellular #status predicted <INT>  
F:465-750/Domain: protein kinase homology <KIN>  
F:473-481/Region: protein kinase ATP-binding motif  
F:57-101,117-224,271-333/disulfide bonds: #status predicted  
F:112-256,290-311,322/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:503,520,612/Active site: Lys, Glu, Asp #status predicted  
F:611,630/Binding site: magnesium (Asn, Asp) #status predicted  
F:643/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

Query Match	20.4%	Score 362.5	DB 1	Length 802
Best Local Similarity	32.38%	Pred. No. 3.1e-18		
Matches 91; Conservative	44;	Mismatches 106;		Indels 41; Gaps 9;

```

QY      61 WTKDRTHTSHCSMRPVLPQC-----LKVKOVEREDAGVYUCKATNGFSLSY--NY 110
Db      66 WKKEGS-----RLAPAGRVGWGRLEITLASFLEPDAFYLCTLAR--GSAITVLQNL 113
QY      111 TLVVLDLDPISPKESLSPDSSGGOEDPA---SOOMARPRFQPSKMRRLYARVGSVSR 167
Db      114 TLITGDSLTLSSNDDPERS-----HRDPENRHSYPOQAAYWHNPQRMKEKLHAYAGNTVK 169
QY      168 LKVASGHPREDITYMKDDQL---TPREALPPKKKKTLSLKLRLREDSGKTYCRVSNR 224
Db      170 FPCPAGAGNPPTIRKLKMGQAFHGENRIGGIRLHQHMSLMESEVSPDSRQTYCLVEMA 229
QY      225 AGAIAATKVVLTIOKTRSKPVLTGSHNPVTVDFGGSFQCKVRSPVKRPVIOQLKRV-- 282
Db      230 VGSIVKNTLVDLDESHPRPLIDQNGLRANTLAAVVGSDVELLCTKYSDAQPHIQMLKIYI 289
QY      283 ---EYGAEG---RHNSTIIDYGQKFVVLPPGDWMSRPGDSY 317
Db      290 NGSSFGAGFPPVYVLKLTADINSSVEVLLYLRNYSABDAGEY 331

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RESULT 24  
S29840  
fibroblast growth factor receptor 1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C.Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C.Accession: S29840  
R.Yazaki, N.; Fujita, H.; Ohta, M.; Kawasaki, T.; Itoh, N.  
Biochim. Biophys. Acta 1172, 37-42, 1993  
A>Title: The structure and expression of the FGF receptor-1 mRNA isoforms in rat tissue  
A.Reference number: S29840; MUID:93176824  
A.Accession: S29840  
A.Status: preliminary  
A.Molecule type: mRNA  
A.Residues: 1-822 <YAA>  
A.Cross-references: EMBL:D12498; NID:q220737; PIDD:BAA02059.1; PID:q220738



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: May 2, 2002, 08:50:24 ; Search time 13.22 Seconds  
(without alignments)  
893.046 Million cell updates/sec

Title: US-09-823-038A-33  
Perfect score: 1779  
Sequence: 1 RRAQCCSCRCRCGSPSHR.....VLPTGVWSRPDGSYLKPL 322

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	391	22.0	801	1	FGR_MOUSE
2	382	21.5	823	1	CEK3_CHICK
3	381.5	21.4	812	1	FGR1_XENLA
4	378	21.2	806	1	FGR3_HUMAN
5	375.5	21.1	806	1	CEK2_CHICK
6	371.5	20.9	821	1	FGR2_HUMAN
7	366.5	20.6	802	1	FGR4_HUMAN
8	364.5	20.5	822	1	FGR1_MOUSE
9	362.5	20.4	822	1	FGR1_RAT
10	361.5	20.3	819	1	FGR1_CHICK
11	361	20.3	821	1	FGR2_MOUSE
12	360.5	20.3	822	1	FGR1_HUMAN
13	358.5	20.2	808	1	FGR4_MOUSE
14	354.5	18.8	813	1	FGR2_XENLA
15	307	17.3	654	1	BFR2_HUMAN
16	254	14.3	2029	1	LAR_DROME
17	243.5	13.7	1052	1	FGR2_DROME
18	225	12.6	1302	1	NRG_DROME
19	224	12.6	3707	1	PGBM_MOUSE
20	222.5	12.5	4393	1	PGBM_HUMAN
21	219.5	12.3	730	1	FGR1_DROME
22	208	11.7	1040	1	EG15_CAEEL
23	207	11.6	1447	1	DCC_HUMAN
24	207	11.6	1447	1	DCC_MOUSE
25	202.5	11.4	1040	1	AXO1_RAT
26	201.5	11.3	1020	1	CONT_MOUSE
27	201.5	11.3	1912	1	PTPD_HUMAN
28	200	11.2	2012	1	DSCA_HUMAN
29	199.5	11.2	853	1	NCAL_BOVIN
30	198.5	11.2	1914	1	KMLS_HUMAN
31	197.5	11.1	1018	1	CONT_HUMAN
32	193.5	10.9	1040	1	AXO1_HUMAN
33	193.5	10.9	1906	1	KMLS_CHICK

34	192.5	10.8	1010	1	CONT_CHICK	p14781 gallus gall
35	191.5	10.8	1897	1	PTPE_HUMAN	p10586 homo sapien
36	191	10.7	1091	1	NCAL_CHICK	p13590 gallus gall
37	190.5	10.7	838	1	NCAL_RAT	p13596 rattus norv
38	190.5	10.7	1051	1	PTK7_CHICK	q91048 gallus gall
39	190	10.7	761	1	NCAL2_HUMAN	p13592 homo sapien
40	190	10.7	848	1	NCAL_HUMAN	p13591 homo sapien
41	190	10.7	898	1	FAS2_SCHAM	p22648 schistocerc
42	185.5	10.4	1070	1	PTK7_HUMAN	q13308 homo sapien
43	182.5	10.3	725	1	NCAL2_MOUSE	p13594 mus musculu
44	182.5	10.3	1115	1	NCAL_MOUSE	p13595 mus musculu
45	180	10.1	1036	1	AXO1_CHICK	p28688 gallus gall
46	180	10.1	1284	1	NRCA_CHICK	p35331 gallus gall
47	174	9.8	811	1	FS22_DROME	p34083 dtrosophila
48	174	9.8	873	1	FS21_DROME	p34082 dtrosophila
49	168	9.4	837	1	NCM2_MOUSE	q35136 mus musculu
50	165.5	9.3	837	1	NCM2_HUMAN	p13594 mus musculu
51	165.5	9.3	1257	1	CAML_HUMAN	p32004 homo sapien
52	163.5	9.2	338	1	LAMP_HUMAN	q13449 homo sapien
53	163.5	9.2	1493	1	NEO1_MOUSE	p97798 mus musculu
54	162.5	9.1	1259	1	CAML_RAT	q05695 rattus norv
55	162	9.1	1461	1	NEO1_HUMAN	q92859 homo sapien
56	161.5	9.1	521	1	BGP1_MOUSE	p31809 mus musculu
57	161.5	9.1	1260	1	CAML_MOUSE	p11627 mus musculu
58	160.5	9.0	338	1	LAMP_RAT	q62813 rattus norv
59	160.5	9.0	1142	1	MYPE_HUMAN	q14324 homo sapien
60	158.5	8.9	359	1	LACH_DROME	q24372 dtrosophila
61	158.5	8.9	1092	1	NCAL2_XENLA	p36335 xenopus lae
62	158.5	8.9	1333	1	VGRI_MOUSE	p35969 mus musculu
63	157	8.8	1356	1	VGRI_HUMAN	p35968 homo sapien
64	157	8.8	1377	1	NEO1_RAT	p97603 rattus norv
65	156.5	8.8	1465	1	MYM2_HUMAN	p54296 homo sapien
66	156	8.8	1266	1	NGCA_CHICK	q03696 gallus gall
67	155.5	8.7	1088	1	NCAL_XENLA	p16170 xenopus lae
68	155.5	8.7	1363	1	VGRI_MOUSE	p35917 mus musculu
69	154.5	8.7	338	1	LAMP_CHICK	q98919 gallus gall
70	154.5	8.7	1176	1	KMLS_BOVIN	q28824 bos taurus
71	154.5	8.7	1336	1	VGRI_RAT	p53767 rattus norv
72	154	8.7	1147	1	KMLS_RABIT	p29294 ocyctolagus
73	152.5	8.6	349	1	LACH_SCHAM	q26474 schistocerc
74	152.5	8.6	626	1	MAG_HUMAN	p20916 homo sapien
75	151	8.5	626	1	MAG_MOUSE	p20917 mus musculu
76	149	8.4	1443	1	NEO1_CHICK	q90610 gallus gall
77	148.5	8.3	626	1	MAG_RAT	p07722 rattus norv
78	146	8.2	333	1	AMAL_DROME	p15366 dtrosophila
79	145.5	8.2	1338	1	VGRI_HUMAN	p17948 homo sapien
80	145.5	8.2	1367	1	VGRI_MOUSE	p35918 mus musculu
81	144.5	8.1	2481	1	UN52_CAEEL	q06561 caenorhabdi
82	144	8.1	537	1	MYPH_CHICK	q05623 gallus gall
83	144	8.1	739	1	VCAL_RAT	p29534 rattus norv
84	142.5	8.0	243	1	CAVT_BRALA	p05548 btanchiosteo
85	142.5	8.0	620	1	SMP_COTUA	q92124 coturnix co
86	142	8.0	353	1	CEPU_CHICK	q00773 gallus gall
87	141.5	8.0	1141	1	MYPS_HUMAN	q00872 homo sapien
88	140.5	7.9	975	1	KKIT_MOUSE	p05532 mus musculu
89	139	7.8	344	1	MYRI_RAT	q62718 rattus norv
90	139	7.8	1271	1	MYPC_CHICK	q90688 gallus gall
91	138.5	7.8	519	1	ECTO_RAT	p16573 rattus norv
92	138	7.8	621	1	MYPS_RAT	q63518 rattus norv
93	137	7.7	739	1	VCAL_MOUSE	p29533 mus musculu
94	136.5	7.7	1131	1	MYPE_CHICK	p16419 gallus gall
95	136.5	7.7	1298	1	VGRI_HUMAN	p35916 homo sapien
96	136	7.6	402	1	RAGE_RAT	q63495 rattus norv
97	135.5	7.6	978	1	KKIT_CAHVI	q28313 capra hircu
98	135.5	7.6	1343	1	MPSE_RAT	q00875 rattus norv
99	134.5	7.6	1450	1	MYPH_CHICK	q02173 gallus gall
100	134	7.5	484	1	MYPH_RAT	q08559 rattus norv

ALIGNMENTS

RESULT 1

FGF3\_MOUSE STANDARD: PRT: 801 AA.

AC 061851: 063834: 35, Created

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (FGFR-3)

GN FGF3 OR MFR3 OR SAM3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=92355591; PubMed=1379594;

RT Ornitz D.M., Leder P.;

RT "Ligand specificity and heparin dependence of fibroblast growth factor receptors 1 and 3."

RL J. Biol. Chem. 267:16305-16311(1992).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=93177694; PubMed=8382556;

RT Katon O., Hattori Y., Sasaki H., Sakamoto H., Fujimoto K.,

RT "Isolation of the complementary DNA encoding a mouse heparin-binding growth factor receptor with the use of a unique kinase insert sequence."

RT Cancer Res. 53:11136-1141(1993).

CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS. PREFERENTIALLY BINDS ACIDIC FGF.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: IN EMBRYO, EXPRESSED IN HEART, LUNG, KIDNEY, SKIN, HEAD AND LIVER BUT NOT IN MUSCLE. IN ADULT, HIGHEST LEVELS IN BRAIN. ALSO EXPRESSED IN LIVER, LUNG, KIDNEY, TESTIS, OVARY AND UTERUS. VERY LOW LEVELS IN HEART, THYMUS, SPLEEN AND MUSCLE.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYO FROM MID-GESTATION AND IN ADULT.

CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR FAMILY.

CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC EMBL: M81342; AAA39535.1; -

DR EMBL: S56291; AAB25535.1; -

DR HSSP: P11362; 1FGL.

DR MGD: MGI:95524; Fgfr3.

DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003598; Ig\_C2.

DR InterPro: IPR001245; Tyr\_kin.

DR Pfam: PF00047; Ig\_3.

DR Pfam: PF00069; pkinase\_1.

DR PRINTS: PR00109; TYRKINASE.

DR SMART: SM00408; IGC2; 3.

DR SMART: SM00219; Tyrc; 1.

DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.

KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transferrase; Phosphorylation; Transmembrane; Immunoglobulin domain; Signal.

KW SIGNAL

FT 1 20 POTENTIAL.

FT CHAIN 21 801 FIBROBLAST GROWTH FACTOR RECEPTOR 3.

FT DOMAIN 21 369 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 370 390 POTENTIAL.

FT DOMAIN 391 801 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 52 114 IG-LIKE C2-TYPE DOMAIN 1.

FT DOMAIN 163 229 IG-LIKE C2-TYPE DOMAIN 2.

FT DOMAIN 262 340 IG-LIKE C2-TYPE DOMAIN 3.

FT DOMAIN 466 756 PROTEIN KINASE.

FT NE\_BIND 472 481 ATP (BY SIMILARITY).

FT BINDING 502 502 ATP (BY SIMILARITY).

FT ACT\_SITE 611 611 BY SIMILARITY.

FT MOD\_RES 642 642 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT DISULFID 59 107 POTENTIAL.

FT DISULFID 170 222 POTENTIAL.

FT DISULFID 269 333 POTENTIAL.

FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 684 684 P -> L (IN REF. 2).

FT CONFLICT 687 687 MISSING (IN REF. 2).

SO SEQUENCE 801 AA; 87758 MW; 68BC110212691705 CRC64;

Query Match 22.0%; Score 391; DB 1; Length 801;

Best Local Similarity 32.1%; Pred. No. 2,8e-22;

Matches 102; Conservative 50; Mismatches 132; Indels 34; Gaps 9;

QY 5 CCSCRCRCWCWSPSHRPPPEAPQFRWRTRWSHGRWAGPHCA-----AVEVEG 54

DB 6 CVLFEVAVAGATSTSPPEDEQVVARAAVEPPEPESQEOVAFSGDVIYELSCHPPGA 65

QY 55 PPELTMTDGRTHSGMSFRVLPGLKVKOVERDAGVYC--KATNGFSLSVNYTL 112

DB 66 PPGPTWADGGLVLS--HRLVGPORLOVLNASHDAGVYSCOHRLTR---RVLCHEFSV 121

QY 113 VVLDIDSPKESIGPPSSSGGDEPFASSQGMARFRFOPSKMRRTVARYVSSVRLKVA 172

DB 122 RYTDASSSGDEDEGEVA-----EDIGAPVY-----TRPERMDKLLAVAAATVRCFA 172

QY 173 SGHPREDITWMDQALT--RPEAEPKKRWTLISLKLREDSGKYCYRYSNRAGAIN 229

DB 173 AGNPPTSIWKLKNGKFEHRIIGIKLRHQWSLYMESVPSDRGNTCYVENKRGISIR 232

QY 230 AITYKVIVIRTSKPYLTGTHVNTVDGTTSTFOCKYRSVYKPYTOMLKRYEIGAEGR 289

DB 233 QYTTLDVLEERSPHRPLIQAQLPANTAILGSDVEFCKVYSDAOPRIOWLKHYEV----- 287

QY 290 HNSTIDVGQKPY-VLPT 306

DB 288 NGSKVGPGSTPYVTYVLT 305

RESULT 2

CEK3\_CHICK STANDARD: PRT: 823 AA.

AC P18461: 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE TYROSINE KINASE RECEPTOR CEK3 PRECURSOR (EC 2.7.1.112).

GN CEK3.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=90332672; PubMed=2165604;

Pasquale E.B.;





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FT CHAIN 21 812 FIBROBLAST GROWTH FACTOR RECEPTOR 1.
FT DOMAIN 21 371 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 372 393 POTENTIAL.
FT DOMAIN 394 812 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 47 107 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 167 233 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 266 344 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 472 761 PROTEIN KINASE.
FT NP_BIND 478 486 ATP (BY SIMILARITY).
FT BINDING 508 508 ATP (BY SIMILARITY).
FT ACT_SITE 617 617 BY SIMILARITY.
FT MOD_RES 648 648 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 812 AA; 90502 MM; B06333BAFEAC5C9B CRC64;

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Query Match 21.4%; Score 381.5; DB 1; Length 812;
Best Local Similarity 31.5%; Pred. No. 1.5e-21;
Matches 95; Conservative 56; Mismatches 128; Indels 23; Gaps 10;

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QY 20 RPP---PPEAPQRMRTMWSGRRPAGHCANPVEDPPRLMTWTGRTIHSGMSRRF 76
DB 22 RPPSTLDEAPAPKTEVEPYSAOPGRITLQCLREDVOSIN-WVKNQVOL-SETNRT 79
QY 77 VLPQGLKVKOVERADGVYCKATNGEGLSVNVTL---VLDDISGKSLGPDSSSG 133
DB 80 ITGEEIOLISAGBEDNNGVYAC-VTNG---PSRRTYGLCSVNSDALPSAEDDDDDDNSS 135
QY 134 QEDPASQOWA--RPRFTOPSKRRRTIARPYGVSSRLKCVASGHPREDITWMKDDQALTR 191
DB 136 SEEKAENSKRNPRLMWSHPKMEKILHAIPAATKVRCPANGPTPTLMLKNNRAFOQ 195
QY 192 PE---AAEPKKKWTLSLKLRLPREDSGKYTCRNSRAGALNATYKVIVORTSKRPVLTG 248
DB 196 DQRIIGYKVSQWTLMDVSVPSDKGNYTCIYENKYGALNHVYOLIVRSPRPILQA 255
QY 249 THPVNTTVDEGCTTSPQCKRSDVKPVYIOWLKRVEYGAEGRHNSITIDVGOKFY-VLPTG 307
DB 256 GLPANTSVTYGTAEESCKKYSDQPHIQMLRIET-----NGSRVASDGPYVEILLKTA 310
Y 308 DV 309
DB 311 GV 312

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RESULT 4
FGR3_HUMAN STANDARD; PRT; 806 AA.
ID FGR3_HUMAN P22607; Q16294; Q14308;
AC 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (BC 2.7.1.112) (FGFR-3).
GN FGR3 OR JTK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
ON NCBI_TaxID=9606;
RX MEDLINE-95400307; PubMed-7670477;
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RA MEDLINE-91142118; PubMed-1847508;
RA Keegan K., Johnson D.E., Williams L.T., Hayman M.J.;
RT Isolation of an additional member of the fibroblast growth factor
RT receptor family, FGFR-3.;

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RL Proc. Natl. Acad. Sci. U.S.A. 88:1095-1099(1991).
RN [2]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RA Terada M., Shimizu A., Seo M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 76-806 FROM N.A. (LONG ISOFORM), AND TISSUE SPECIFICITY.
RC TISSUE=Fetal brain;
RX MEDLINE-92147110; PubMed-1664411;
RA Thompson L.M., Plummer S., Schalling M., Altherr M.R., Gusella J.F.,
RA Housman D.E., Wasmuth J.U.;
RT "A gene encoding a fibroblast growth factor receptor isolated from the
RT Huntington disease gene region of human chromosome 4.";
RN Genomics 11:1133-1142(1991).
RN [4]
RP SEQUENCE OF 614-681 FROM N.A.
RX MEDLINE-91062389; PubMed-2247464;
RA Partanen J., Maekela T.P., Allitalo R., Lehtvaesialho H.,
RA Allitalo K.;
RT "Putative tyrosine kinases expressed in K-562 human leukemia cells.";
RN Proc. Natl. Acad. Sci. U.S.A. 87:8913-8917(1990).
RN [5]
RP VARIANT ACH ARG-380.
RX MEDLINE-94359611; PubMed-8078586;
RA Rousseau F., Bonaventure J., Legault-Mallet L., Pelet A., Rozet J.-M.,
RA Martoreaux P., Le Merrer M., Munnich A.;
RT "Mutations in the gene encoding fibroblast growth factor receptor-3
RT in achondroplasia.";
RL Nature 371:252-254(1994).
RN [6]
RP VARIANT ACH ARG-380.
RX MEDLINE-95150025; PubMed-7847369;
RA Bellus G.A., Hefferon T.W., de Luna R.I., Hecht J.T., Horton W.A.,
RA Machado M., Kaitila I., McIntosh I., Francomano C.A.;
RT "Achondroplasia is defined by recurrent G380R mutations of FGFR3.";
RL Am. J. Hum. Genet. 56:368-373(1995).
RN [7]
RP VARIANT ACH CYS-375.
RX MEDLINE-95278277; PubMed-7758520;
RA Supertli-Furga A., Eich G., Bucher H.U., Wisser J., Gledion A.,
RA Gitzelmann R., Steinmann B.;
RT "A glycine 375-to-cysteine substitution in the transmembrane domain
RT of the fibroblast growth factor receptor-3 in a newborn with
RT achondroplasia.";
RL Eur. J. Pediatr. 154:215-219(1995).
RN [8]
RP VARIANT TD1 CYS-249.
RX MEDLINE-96154693; PubMed-8589699;
RA Tavorimla P.L., Rimoin D.L., Conn D.H., Zhu Y.-Z., Shiang R.,
RA Wasmuth J.U.;
RT "Another mutation that results in the substitution of an unpaired
RT cysteine residue in the extracellular domain of FGFR3 in
RT thanatophoric dysplasia type I.";
RL Hum. Mol. Genet. 4:2175-2177(1995).
RN [9]
RP VARIANTS TD1 CYS-248 AND CYS-371, AND VARIANT TD2 GLU-650.
RX MEDLINE-95291326; PubMed-7773297;
RA Tavorimla P.L., Shiang R., Thompson L.M., Zhu Y.-Z., Wilkin D.J.,
RA Lachman R.S., Wilcox W.R., Rimoin D.L., Conn D.H., Wasmuth J.U.;
RT "Thanatophoric dysplasia (types I and II) caused by distinct
RT mutations in fibroblast growth factor receptor 3.";
RL Nat. Genet. 9:321-328(1995).
RN [10]
RP VARIANT HYPOCHONDROPLASIA LYS-540.
RX MEDLINE-95400307; PubMed-7670477;
RA Bellus G.A., McIntosh I., Smith E.A., Aylsworth A.S., Kaitila I.,
RA Horton W.A., Greenhaw G.A., Hecht J.T., Francomano C.A.;
RT "A recurrent mutation in the tyrosine kinase domain of fibroblast
RT growth factor receptor 3 causes hypochondroplasia.";
RL Nat. Genet. 10:357-359(1995).
RN [11]
RP VARIANT CROUZON GLU-391.
RX MEDLINE-96083601; PubMed-7493034;

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RA Meyers G.A., Orlow S.J., Munro I.R., Przylepka K.A., Jabs E.W.;  
RT "Fibrolast growth factor receptor 3 (FGFR3) transmembrane mutation  
RT in Crozon syndrome with acanthosis nigricans.";  
RL Net. Genet. 11:462-464(1995).  
RN [12]  
RN CHARACTERIZATION OF VARIANT ACH ARG-380.  
RP MEDLINE=96174812; PubMed=8599935;  
RX Webster M.K., Donoghue D.J.;  
RA "Constitutive activation of fibroblast growth factor receptor 3 by  
RA le Merrier M., Munnich A., Bonaventure J.;  
RT "Missense FGFR3 mutations create cysteine residues in thanatophoric  
RT dwarfism type I (TDI).";  
RL Hum. Mol. Genet. 5:509-512(1996).  
RN [14]  
RN VARIANT CRS3 ARG-250.  
RP MEDLINE=97195541; PubMed=9042914;  
RX Muenke M., Gripp K.W., McDonald-McGinn D.M., Gaudenz K.,  
RA Whitaker L.A., Bartlett S.P., Markowitz R.I., Robin N.H., Nwokoro N.,  
RA Milroy R.S., Clarke L.A., Hollway G., Ades L.C., Haan E.A.,  
RA Mulvey J.C., Cohen M.M., Jr., Bellus G.A., Franccomano C.A.,  
RA Moloney D.M., Wall S.A., Wilkie A.O.M., Zackai E.H.;  
RT "A unique point mutation in the fibroblast growth factor receptor 3  
RT gene (FGFR3) defines a new craniosynostosis syndrome.";  
RL Am. J. Hum. Genet. 60:555-564(1997).  
RN [15]  
RN VARIANT TDI CYS-370.  
RP MEDLINE=99004917; PubMed=9790257;  
RX Katsunata N., Kuno T., Miyazaki S., Mikami S., Nagashima-Miyokawa A.,  
RA Nishura A., Horikawa R., Tanaka T.;  
RT "G370G mutation in the FGFR3 gene in a Japanese patient with  
RL thanatophoric dysplasia.";  
RL Endocr. J. 45:5171-5174(1998).  
RN [16]  
RN VARIANT HYPOCHONDROPLASIA VAL-538.  
RP Grigeliioniene G., Haganaes L., Ekloef O., Neumeyer L., Haereld P.E.,  
RA Anvret M.;  
RT "A novel missense mutation Ile538Val in the fibroblast growth  
RT factor receptor 3 in hypochondroplasia.";  
RL Hum. Mutat. 11:333-333(1998).  
RN [17]  
RN VARIANT HYPOCHONDROPLASIA THR-540.  
RP MEDLINE=98112422; PubMed=9452043;  
RX Deutz-Terlow P.P., Losekoot M., Aalfs C.M., Hennekam R.C.M.,  
RA Bakker E.;  
RT "Asn540Thr substitution in the fibroblast growth factor receptor 3  
RT tyrosine kinase domain causing hypochondroplasia.";  
RL Hum. Mutat. Suppl. 1:562-S65(1998).  
RN [18]  
RN VARIANT TDI MET-650.  
RA Kitchin H., Brodie S.G., Kupke K.G., Lachman R.S., Wilcox W.R.;  
RT "Lys650Met substitution in the tyrosine kinase domain of the  
RT fibroblast growth factor receptor gene causes thanatophoric dysplasia  
RT type I.";  
RL Hum. Mutat. 12:362-363(1998).  
CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH  
CC FACTORS. PREFERENTIALLY BINDS ACIDIC EGF.  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
CC TYROSINE PHOSPHATE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, KIDNEY AND TESTIS. VERY  
CC LOW OR NO EXPRESSION IN SPLEEN, HEART, AND MUSCLE. IN 20-TO 22-  
CC WEEK OLD FETUSES IT IS EXPRESSED AT HIGH LEVEL IN KIDNEY, LUNG,  
CC SMALL INTESTINE AND BRAIN, AND TO A LOWER DEGREE IN SPLEEN, LIVER  
CC AND MUSCLE.

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-1- DISEASE: DEFECTS IN FGFR3 ARE THE CAUSE OF THE CRANIOFACIAL
CC DOMINANT DISEASE ACHONDROPLASIA (ACH): THE MOST FREQUENT FORM OF
CC SHORT-LIMB DWARISM. ACH IS CHARACTERIZED BY A LONG, NARROW TRUNK,
CC SHORT EXTREMITIES, PARTICULARLY IN THE PROXIMAL (RHIZOMELIC)
CC SEGMENTS, A LARGE HEAD WITH FRONTAL BOWING, HYPOPLASIA OF THE
CC MIDFACE AND A TRIDENT CONFIGURATION OF THE HANDS.
CC -1- DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF CROUZON SYNDROME, ALSO
CC CALLED CRANIOFACIAL DYSOSTOSIS TYPE I (CFDI). CHARACTERIZED BY
CC CRANIOSYNOSTOSIS (PREMATURE FUSION OF THE SKULL SUTURES),
CC HYPERTELORISM, EXOPHTHALMOS AND EXTERNAL STRABISMUS, PARROT-BEAKED
CC NOSE, SHORT UPPER LIP, HYPOPLASTIC MAXILLA, AND A RELATIVE
CC MANDIBULAR PROGNATHISM.
CC -1- DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF THANATOPHORIC DYSPLASIA
CC (TD) (ALSO KNOWN AS THANATOPHORIC DWARISM), THE MOST COMMON
CC NEONATAL LETHAL SKELETAL DYSPLASIA, AFFECTED INDIVIDUALS DISPLAY
CC FEATURES SIMILAR TO THOSE SEEN IN HOMOZYGOUS ACHONDROPLASIA. IT
CC CAUSES SEVERE SHORTENING OF THE LIMBS WITH MACROCEPHALY, NARROW
CC THORAX AND SHORT RIBS. IN THE MOST COMMON SUBTYPE (TD1), FEMUR ARE
CC CURVED, WHILE IN TD2, STRAIGHT FEMURS ARE ASSOCIATED WITH
CC CLOVERLEAF SKULL.
CC -1- DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF CRANIOSYNOSTOSIS ADELAIDE
CC TYPE (CRS3). A FORM OF CORONAL SYNOSTOSIS (CS) CHARACTERIZED BY
CC CRANIOSYNOSTOSIS, MIDFACE HYPOPLASIA, DOWNSLANDING PALPEBRAL
CC FISSURES, PROTUS, HIGHLY ARCHED PALATE, MID-TO-MODERATE
CC SENSORINEURAL HEARING LOSS, NORMAL STATURE, BRADYDACTYL, BROAD
CC BIG TOES. RADIOLOGICALLY, HANDS AND FEET SHOW THIMBLE-LIKE MIDDLE
CC PHALANXES, CONED EPIPHYSES, AND CARPAL AND TARSAL FUSIONS.
CC -1- DISEASE: DEFECTS IN FGFR3 ARE A CAUSE OF THE AUTOSOMAL DOMINANT
CC DISEASE HYPOCHONDROPLASIA CHARACTERIZED BY DISPROPORTIONATE SHORT
CC STATURE. IT RESEMBLES ACHONDROPLASIA, BUT WITH A LESS SEVERE
CC PHENOTYPE.
CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR
CC FAMILY.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC
Query Match 21.2%, Score 378; DB 1; Length 806;
Best Local Similarity 31.8%; Pred. No. 2,76-21;
Matches 96; Conservative 54; Mismatches 118; Indels 34; Gaps 10;

16 GSHNRPPEAPQQRRTMSHGRWAGHCAAAVVEEDPP--PL--TMMTKDGRTIHS 70
Db 33 GRAAVVPPEPEQEQQLVFGSG-----DAVELSCPPPEGGPMGTVMWKDDGTGLVP 83
QY 71 GWSRFRVLPQGLKYNQVERDAGVYVC--KATNGFGLSVNVTLLVLDISPGEKSLAPD 128
Db 84 S-ERVLVGPRLQVLNASHEDSGAVSCHORLTO--RVLCHEVSVMVTADPSSGDDEDED 139
QY 129 SSSGGQEPASQAMARPFETQPSKKRRVIARPVSSVRLKCVASGHRPRDITMMKKDOA 188
Db 140 EAEDTGVNLTGARVW----TRPERDKKLLVPAANTVAFRCRPAAGNPTPSIWLKNRE 194
QY 189 LT---RPEAAPEKKKWTLSLKNLPEESGKTYCVSRACAGINTATYKVDVIQFRSKPV 245
Db 195 FRGEHRIGIGIKIRHQMSLWMSVYSPDRGNTTYEVEKKFGSIRRTYLLDLIELSRPHPI 254
QY 246 LTGTHPVNTTVDFGGTTSFOCKVRSRVKRVQIWLKRVYGAEGRRNSTIDVGQKRV-VL 304
Db 255 LQAGLRPAQGTAVLGSDVFEHCKVYDDAQRPHIOLKNHEV-----NGSKVGPDGTFYTVL 309
QY 305 PT 306
Db 310 KT 311

RESULT 5
ID_CERK2_CHICK STANDARD: PRT: 806 AA.
AC PI460;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)

```



- RL Proc. Natl. Acad. Sci. U.S.A. 87:5983-5987(1990).
- RN [5] VARIANTS FROM N.A.
- RP MEDLINE-92212948; PubMed-1313574;
- RX Kato M., Hattori Y., Sasaki H., Tanaka M., Sugano K., Yazaki Y.,
- RA Sugimura T., Terada M.;
- RT "x-sam gene encodes secreted as well as transmembrane receptor
- RT tyrosine kinase.";
- RL Proc. Natl. Acad. Sci. U.S.A. 89:2960-2964(1992).
- RN [6] SEQUENCE FROM N.A.
- RP TISSUE-Placenta;
- RX MEDLINE-93016048; PubMed-1400433;
- RA Dell K.R., Williams L.T.;
- RT "A novel form of fibroblast growth factor receptor 2. Alternative
- RT splicing of the third immunoglobulin-like domain confers ligand
- RT binding specificity.";
- RL J. Biol. Chem. 267:21225-21229(1992).
- RN [7] SEQUENCE FROM N.A.
- RP TISSUE-Blood;
- RA Steinberger D., Mueller U.;
- RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
- RN [8] VARIANTS CS HIS-340; ARG-342; SER-342; TYR-342 AND CYS-354.
- RP MEDLINE-95078932; PubMed-7987400;
- RX Reardon W., Winter R.M., Rutland P., Pulley L.J., Jones B.M.,
- RA Malcolm S.;
- RT "Mutations in the fibroblast growth factor receptor 2 gene cause
- RT Crozon syndrome.";
- RL Nat. Genet. 8:98-103(1994).
- RN [9] VARIANTS CS CYS-328 AND CYS-347, AND VARIANT JWS GLY-344.
- RP MEDLINE-9519174; PubMed-874170;
- RX Jabs E.W., Li X., Scott A.F., Meyers G., Chen W., Eccles M., Mao J.,
- RA Charles L.R., Jackson C.E., Jaye M.;
- RT "Jackson-Weiss and Crozon syndromes are allelic with mutations in
- RT fibroblast growth factor receptor 2.";
- RL Nat. Genet. 8:275-279(1994).
- RN [10] VARIANTS CS.
- RP MEDLINE-95384152; PubMed-7655462;
- RX Oldridge M., Wilkie A.O.M., Stanley S.F., Poole M.D., Pulley L.J.,
- RA Rutland P., Hockley A.D., Wake M.J.C., Goldin J.H., Winter R.M.,
- RA Reardon W., Malcolm S.;
- RT "Mutations in the third immunoglobulin domain of the fibroblast growth
- RT factor receptor-2 gene in Crozon syndrome.";
- RL Hum. Mol. Genet. 4:1077-1082(1995).
- RN [11] VARIANTS PS ALA-321.
- RP MEDLINE-95235551; PubMed-7719333;
- RX Lejeune E., Wei M.H., Bonaventure J., Munnich A., le Merrier M.,
- RA Renier D.;
- RT "FGFR2 mutations in Pfeiffer syndrome.";
- RL Nat. Genet. 9:108-108(1995).
- RN [12] VARIANTS AS TRP-252 AND ARG-253.
- RP MEDLINE-95235562; PubMed-7719344;
- RX Wilkie A.O.M., Stanley S.F., Oldridge M., Poole M.D., Ashworth G.J.,
- RA Hockley A.D., Hayward R.D., David D.J., Pulley L.J., Rutland P.,
- RA Malcolm S., Winter R.M., Reardon W.;
- RT "Aper syndrome results from localized mutations of FGFR2 and is
- RT allelic with Crozon syndrome.";
- RL Nat. Genet. 9:165-172(1995).
- RN [13] VARIANTS PS PRO-341; ARG-342 AND TYR-342.
- RP MEDLINE-95235563; PubMed-7719345;
- RX Rutland P., Pulley L.J., Reardon W., Baraister M., Hayward R.,
- RA Jones B., Malcolm S., Winter R.M., Oldridge M., Stanley S.F.,
- RA Poole M.D., Wilkie A.O.M.;
- RT "Identical mutations in the FGFR2 gene cause both Pfeiffer and
- RT Crozon syndrome phenotypes.";
- RL Nat. Genet. 9:173-176(1995).
- RN [14] VARIANTS CS/JWS/PS.
- RP MEDLINE-96203627; PubMed-8644708;
- RX Meyers G.A., Day D., Goldberg R., Daentli D.L., Przybyla K.A.,
- RA Abrams L.J., Graham J.M. Jr., Feingold M., Moeschler J.B.,
- RA Ramsley E., Scott A.F., Jabs E.W.;
- RT "FGFR2 exon IIIa and IIc mutations in Crozon, Jackson-Weiss, and
- RT Pfeiffer syndromes: evidence for missense changes, insertions, and a
- RT deletion due to alternative RNA splicing.";
- RL Am. J. Hum. Genet. 58:491-498(1996).
- RN [15] VARIANTS CS CYS-105; GLU-338; CYS-351 AND ARG-384.
- RP MEDLINE-97101656; PubMed-8946174;
- RX Pulley L.J., Reardon W., Wilkes D., Rutland P., Jones B.M.,
- RA Hayward R., Hall C.M., Brunton L., Chun N., Lammner E., Malcolm S.,
- RA Winter R.M.;
- RT "Spectrum of craniosynostosis phenotypes associated with novel
- RT mutations at the fibroblast growth factor receptor 2 locus.";
- RL Eur. J. Hum. Genet. 4:283-291(1996).
- RN [16] VARIANTS CS ILE-331; ASP-336--ALA-337 DUPL AND TRP-356--THR-358 DEL.
- RP MEDLINE-97114301; PubMed-8956050;
- RX Steinberger D., Mulliken J.B., Mueller U.;
- RT "Crozon syndrome: previously unrecognized deletion, duplication, and
- RT point mutation within FGFR2 gene.";
- RL Hum. Mutat. 8:386-390(1996).
- RN [17] VARIANTS PS CYS-290.
- RP MEDLINE-97295073; PubMed-9150725;
- RX Tartaglia M., Valeri S., Velardi F., di Rocco C., Battaglia P.A.;
- RT "Trp290Cys mutation in exon IIIa of the fibroblast growth factor
- RT receptor 2 (FGFR2) gene is associated with Pfeiffer syndrome.";
- RL Hum. Genet. 99:602-606(1997).
- RN [18] VARIANTS CS L-252, VARIANT AS F-252, AND VARIANT PS F-252-S-253.
- RP MEDLINE-97156222; PubMed-9002682;
- RX Oldridge M., Lunt P.W., Zackai E.H., McDonald-McGinn D.M., Muenke M.,
- RA Moloney D.M., Twigg S.R.F., Heath J.K., Howard T.D., Hoganson G.,
- RA Gagnon D.M., Jabs E.W., Wilkie A.O.M.;
- RT "Genotype-phenotype correlation for nucleotide substitutions in the
- RT Igit-Igit linker of FGFR2.";
- RL Hum. Mol. Genet. 6:137-143(1997).
- RN [19] VARIANTS CS GLU-292.
- RP MEDLINE-97297373; PubMed-9152842;
- RX Steinberger D., Collmann H., Schmalenberger B., Mueller U.;
- RT "A novel mutation (a886g) in exon 5 of FGFR2 in members of a family
- RT with Crozon phenotype and plagiocephaly.";
- RL J. Med. Genet. 34:420-422(1997).
- RN [20] VARIANTS CS VAL-276; CYS-301 AND SER-314.
- RP MEDLINE-98180879; PubMed-9521581;
- RX Steinberger D., Vriend G., Mulliken J.B., Mueller U.;
- RT "The mutations in FGFR2-associated craniosynostoses are clustered in
- RT five structural elements of immunoglobulin-like domain III of the
- RT receptor.";
- RL Hum. Genet. 102:145-150(1998).
- RN [21] VARIANTS AS TRP-252 AND ARG-253.
- RP MEDLINE-98112406; PubMed-9452027;
- RX Tsai F.-J., Hwu W.-L., Lin S.-P., Chang J.-G., Wang T.-R., Tsai C.-H.;
- RT "Two common mutations 934C to G and 937C to G of fibroblast growth
- RT factor receptor 2 (FGFR2) gene in Chinese patients with Aper
- RT syndrome.";
- RL Hum. Mutat. Suppl. 1:S18-S19(1998).
- RN [22] VARIANTS PS CYS-351.
- RP MEDLINE-98358420; PubMed-9693549;
- RX Mathijssen I.M., Vaandrager J.M., Hoogheboom A.J.,
- RA Hesselink-Janssen A.L., van den Ouweland A.M.W.;
- RT "Pfeiffer's syndrome resulting from an S351C mutation in the
- RT fibroblast growth factor receptor-2 gene.";
- RL J. Craniofac. Surg. 9:207-209(1998).



SQ SEQUENCE 802 AA; 87954 MW; B22B259831BB889F CRC64;  
 Query Match 20.6%; Score 366.5; DB 1; Length 802;  
 Best Local Similarity 32.3%; Pred. No. 2e-20;  
 Matches 91; Conservative 45; Mismatches 105; Indels 41; Gaps 9;  
 61 WTKGRTTHSGMSRFRVLPQG-----LKVQVEREDAGVYCKAKNGSGLSV--NY 110  
 66 WYKGG-----RLAPAGRVGWRGRLEIASFLPEDAGRYCLAR--GSMIVLONL 113  
 111 TLVLVDLDPKESLGPSSSGQEDPA---SQOWARFRPOPSKMRRIARIPGSSVR 167  
 114 TLILGDLTSSNDEDEPR-----HRDPSNRHSYPOQAPYWHHPQMEKKLAIVAGNTVK 169  
 168 LKCAVASHPRDITWMDQDAL---TRPEAAEPRKKWTLSLKLRPDSGKYTCRVSNR 224  
 170 FRCPAGNPTPTIRMLKQCAFHGENRIGGIRLHOHMSLVMSVSPDRGTTCIVENA 229  
 225 AGAINATYKVVDIORTSKPVLITGHNPVNTVDFGCTISPOCKYRSDVKYIOMLKNR-- 282  
 230 VGSIRYNLTLVDLERSRPRPLQAGLPAVNTAVVGSVDVELCKYVSDAOPHIQWLKHTVI 289  
 283 ---EYGAEG---RHNSTIDVGGOKFVLPYGDWVSRRPGSY 317  
 290 NGSSFGADGFPYGVVLTAKADINSSEVEVLRYNVAEDAGRY 331  
 RESULT 8  
 FGRL\_MOUSE STANDARD; PRT; 822 AA.  
 ID FGRL\_MOUSE  
 AC P16092; 001736; 061562;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE BASIC FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (EC 2.7.1.112)  
 DE (FGFR-1) (BFGF-R) (MFR).  
 GN FGFR1 OR FLG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=90160373; PubMed=1689490;  
 RA Reid H.H., Wilks A.F., Bernard O.;  
 RT "Two forms of the basic fibroblast growth factor receptor-like mRNA  
 are expressed in the developing mouse brain."  
 RT Proc. Natl. Acad. Sci. U.S.A. 87:1596-1600(1990).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=BALE/C; TISSUE=Brain;  
 RX MEDLINE=90265603; PubMed=2161096;  
 RA Satrian A., Avivi A., Orr-Urtreger A., Neufeld G., Lona P.,  
 RA Givol D., Yarden Y.;  
 RT "The murine flg gene encodes a receptor for fibroblast growth  
 factor."  
 RT Oncogene 5:635-643(1990).  
 RL [3]  
 RN SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
 RX MEDLINE=91207411; PubMed=1708247;  
 RA Kouhara H., Kasayama S., Saito H., Matsumoto K., Sato B.;  
 RT "Expression cDNA cloning of fibroblast growth factor (FGF) receptor  
 in mouse breast cancer cells: a variant form in FGF-responsive  
 transformed cells."  
 RT Biochem. Biophys. Res. Commun. 176:31-37(1991).  
 RL [4]  
 RP SEQUENCE FROM N.A. (SHORT FORM).  
 RX MEDLINE=90272715; PubMed=2161540;  
 RA Mansukhani A., Moscatelli D., Talarico D., Levytska V., Basillco C.;  
 RT "A murine fibroblast growth factor (FGF) receptor expressed in CHO  
 cells is activated by basic FGF and Kaposi FGF."

Proc. Natl. Acad. Sci. U.S.A. 87:4378-4382(1990).  
 [5]  
 RP SEQUENCE OF 1-15 FROM N.A. AND ALTERNATIVE SPLICING.  
 RX MEDLINE=95100926; PubMed=7802632;  
 RA Harada T., Saito H., Kouhara H., Kurebayashi S., Kasayama S.,  
 RA Terakawa N., Kishimoto T., Sato B.;  
 RT "Murine fibroblast growth factor receptor 1 gene generates multiple  
 messenger RNAs containing two open reading frames via alternative  
 splicing."  
 RL Biochem. Biophys. Res. Commun. 205:1057-1063(1994).  
 CC -1- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR. A SHORTER  
 CC FORM OF THE RECEPTOR COULD BE A RECEPTOR FOR ACIDIC FGF (ARFGF).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN  
 CC TYROSINE PHOSPHATE  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A LONG FORM (SHOWN HERE), A  
 CC VARIANT FORM AND A SHORT FORM ARE PRODUCED BY ALTERNATIVE  
 CC SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
 CC FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; M28998; AAA37290.1; -;  
 DR EMBL; X51893; CAA36175.1; -;  
 DR EMBL; M65053; AAA37620.1; -;  
 DR EMBL; M33760; AAA37622.1; -;  
 DR EMBL; S74765; AAB32845.1; ALT\_SEQ.  
 DR PIR; A34849; TVMSFG.  
 DR HSSP; P11362; IFC1.  
 DR MGI; MGI:95522; Fgfr1.  
 DR InterPro: IPR000719; Euk\_Dkinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR001245; Tyr\_kin.  
 DR Pfam; PF00047; Ig\_3.  
 DR Pfam; PF00069; pkinase.1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR SMART; SM00408; IGC2; 3.  
 DR SMART; SM00219; TYRC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
 KW Transferase; Phosphorylation; Transmembrane; Signal;  
 KW Immunoglobulin domain; Alternative splicing.  
 FT SIGNAL 1 21  
 FT CHAIN 22 822  
 FT 1  
 FT BASIC FIBROBLAST GROWTH FACTOR RECEPTOR  
 FT 1  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM  
 FT DOMAIN 377 397  
 FT DOMAIN 398 822  
 FT DOMAIN 48 108  
 FT DOMAIN 171 237  
 FT DOMAIN 270 348  
 FT DOMAIN 478 767  
 FT NP\_BIND 484 492  
 FT BINDING 514 514  
 FT ACT\_SITE 623 623  
 FT MOD\_RES 654 654  
 FT DISULFID 55 101  
 FT DISULFID 178 230  
 FT DISULFID 277 341  
 FT CARBOHYD 77 77  
 FT CARBOHYD 117 117  
 FT CARBOHYD 227 227  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 264 264 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VASAPLIC 30 30 Q -> QOSSSWPLVAAA (IN VARIANT FORM).  
 FT VASAPLIC 31 31 MISSING (IN SHORT ISOFORM).  
 FT VASAPLIC 148 149 MISSING (IN VARIANT FORM).  
 FT CONFLICT 229 229 T -> S (IN REF. 4).  
 FT CONFLICT 256 258 ILO -> HPS (IN REF. 1 AND 3).  
 FT CONFLICT 270 270 G -> A (IN REF. 4).  
 FT CONFLICT 387 387 I -> M (IN REF. 3).  
 FT CONFLICT 440 440 G -> A (IN REF. 2).  
 FT CONFLICT 508 508 V -> L (IN REF. 3).  
 FT CONFLICT 544 544 I -> M (IN REF. 4).  
 FT CONFLICT 756 756 R -> H (IN REF. 1).  
 FT CONFLICT 765 765 E -> D (IN REF. 4).  
 SQ SEQUENCE 822 AA; 91980 MW; D5A465FA80926B CRC64;

Query Match 20.5%; Score 364.5; DB 1; Length 822;  
 Best Local Similarity 30.6%; Pred. No. 2.9e-20;  
 Matches 90; Conservative 47; Mismatches 106; Indels 51; Gaps 10;

QY 20 RPP--PEAPORRTKRWSHGRMPAGHCAAVPE-----GDPPPLTM-----60  
 DB 22 RAPPLPEQAPW-----GVPVEESLVHPGDLQRLCRDRDQSI 64  
 QY 61 -WTGDS-RTSHGWSRFRVLPGKVKQVERDAGYVVCATNGFSLSVNTLVLDI 118  
 DB 65 NMLRDSVQVLES--NRRITIGEEVEYVDSIPADSGLYACTSSPSGS-DITYFSVNSDA 121  
 QY 119 SPKESLSGPPSSSGGQDPA-----SOOMARPRFOPSKMRRIYAPVSSVRLKCVAS 173  
 DB 122 LPSEDDDDDDSSSEKETDNTKPNRPVAPYWTSPKNEKKLHAPAKTVFKCPSS 181  
 QY 174 GHPRPDITWKKDOALTRPE-----AAEPKKKWTLSKLNRPEDSGKYTCRVSNRAGAIN 229  
 DB 182 GTPPPLTMKNGKEF-KPHRIGIGYKRYATWSINDSVSPKGNVTCIVENEYGSIN 240  
 QY 230 ATYKVDVIGRTSRKPVLTGTHPVNTVDFGTTSFQCKVSDVAPVLOMKRVE 283  
 DB 241 HTYQLDYVERSHPRLIQAGLPLANKYVALGNSVEFMCKVSDPOPHIOMLKHE 294

RESULT 9  
 FGRL\_RAT STANDARD; PRT; 822 AA.  
 AC 004589;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE BASIC FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (EC 2.7.1.112)  
 DE (FGFR-1) (BFGF-R) (MFR).  
 GN FGFR1 OR FIG.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93176824; PubMed=8382532;  
 RA Yasaki N., Hiroko F., Mitsuhiro O., Toshisuke K., Nobuyuki I.;  
 RT "The structure and expression of the fgf receptor-1 mRNA isoforms in rat tissues.";  
 RL Biochim. Biophys. Acta 1172:37-42(1993).  
 CC -1- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR. A SHORTER FORM OF THE RECEPTOR COULD BE A RECEPTOR FOR ACIDIC BFG (ABFG).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR FAMILY.

CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL: D12498; BAA02059.1; -;  
 DR PIR: S29840; S29840.  
 DR HSSP: P11362; IEG1.  
 DR InterPro: IPR000719; Euk\_Pkinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR001245; Tyr\_kin.  
 DR Pfam: PF00047; Ig; 3.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; ICG2; 3.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_APP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; App-binding; Transmembrane; Signal;  
 KW Immunoglobulin domain.  
 FT CHAIN 1 21 POTENTIAL.  
 FT STGNAL 1 21 BASIC FIBROBLAST GROWTH FACTOR RECEPTOR  
 FT 1. EXTRACELLULAR (POTENTIAL).  
 FT 2. TRANSMEM 377 397 POTENTIAL.  
 FT 3. CYTOPLASMIC (POTENTIAL).  
 FT 4. DOMAIN 398 822 IG-LIKE C2-TYPE DOMAIN 1.  
 FT 5. DOMAIN 408 108 IG-LIKE C2-TYPE DOMAIN 2.  
 FT 6. DOMAIN 171 237 IG-LIKE C2-TYPE DOMAIN 3.  
 FT 7. DOMAIN 270 348 PROTEIN KINASE.  
 FT 8. BIND 478 767 APP (BY SIMILARITY).  
 FT 9. BIND 484 492 APP (BY SIMILARITY).  
 FT 10. BIND 514 514 APP (BY SIMILARITY).  
 FT 11. BIND 514 514 APP (BY SIMILARITY).  
 FT 12. BIND 623 623 APP (BY SIMILARITY).  
 FT 13. BIND 623 623 APP (BY SIMILARITY).  
 FT 14. BIND 654 654 APP (BY SIMILARITY).  
 FT 15. BIND 654 654 APP (BY SIMILARITY).  
 FT 16. BIND 101 101 APP (BY SIMILARITY).  
 FT 17. BIND 178 230 APP (BY SIMILARITY).  
 FT 18. BIND 277 341 APP (BY SIMILARITY).  
 FT 19. BIND 341 341 APP (BY SIMILARITY).  
 FT 20. BIND 77 77 APP (BY SIMILARITY).  
 FT 21. BIND 117 117 APP (BY SIMILARITY).  
 FT 22. BIND 227 227 APP (BY SIMILARITY).  
 FT 23. BIND 240 240 APP (BY SIMILARITY).  
 FT 24. BIND 264 264 APP (BY SIMILARITY).  
 FT 25. BIND 296 296 APP (BY SIMILARITY).  
 FT 26. BIND 317 317 APP (BY SIMILARITY).  
 FT 27. BIND 330 330 APP (BY SIMILARITY).  
 FT 28. BIND 330 330 APP (BY SIMILARITY).  
 SQ SEQUENCE 822 AA; 91824 MW; E59D92AD0A1D5C5 CRC64;

Query Match 20.4%; Score 362.5; DB 1; Length 822;  
 Best Local Similarity 30.4%; Pred. No. 4.1e-20;  
 Matches 89; Conservative 44; Mismatches 111; Indels 49; Gaps 9;

QY 20 RPP--PEAPORRTKRWSHGRMPAGHCAAVPE-----GDPPPLTM-----60  
 DB 22 RAPPLPEQAPW-----GVPVEESLVHPGDLQRLCRDRDQSI 64  
 QY 61 -WTGDS-RTSHGWSRFRVLPGKVKQVERDAGYVVCATNGFSLSVNTLVLDI 119  
 DB 65 NMLRDSVQVLES--NRRITIGEEVEYVDSIPADSGLYACTSSPSGS-DITYFSVNSDA 122  
 QY 120 SPKESLSGPPSSSGGQDPA-----SOOMARPRFOPSKMRRIYAPVSSVRLKCVAS 174  
 DB 123 LPSEDDDDDDSSSEKETDNTKPNRPVAPYWTSPKNEKKLHAPAKTVFKCPSSG 182  
 QY 175 GHPRPDITWKKDOALTRPE-----AAEPKKKWTLSKLNRPEDSGKYTCRVSNRAGAIN 230

Db 183 TPSPFLRLKNGKEF-KPDHRIGGYKVRATWSTIMDSVPSDKGNVTCIYENKSGSNH 241  
 QY 231 TYKDVIOFTRSKPVLTGTHPVNTVDFGGTTSPOCKRSDVKRYIOWLKRYE 283  
 Db 242 TYOLDVRSRPHRILOAGLPANKTVAGSNVEFCKVYSDPOPHIOWLKRIE 294

RESULT 10  
 FGRL\_CHICK STANDARD; PRT; 819 AA.  
 AC P21804;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE BASIC FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (EC 2.7.1.112).  
 GN CERI.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 NCBI\_TaxID=9031;  
 RX MEDLINE=9315814; PubMed=2473471;  
 RA Pasquale E.B., Singer S.J.;  
 RT "Identification of a developmentally regulated protein-tyrosine  
 RT kinase by using anti-phosphotyrosine antibodies to screen a cDNA  
 RT expression library.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 86:5449-5453(1989).  
 RN [2]  
 RP REVISIONS.  
 RA Pasquale E.B.;  
 RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89298406; PubMed=254496;  
 RA Lee P.L., Johnson D.E., Consens L.S., Fried V.A., Williams L.T.;  
 RT "Purification and complementary DNA cloning of a receptor for basic  
 RT fibroblast growth factor.";  
 RL Science 245:57-60(1989).  
 CC -1- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
 CC FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
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EMBL; M24637; AAA48663.1; -  
 DR PIR; A41345; TYCHFG.  
 DR HSSP; P11362; IFGI.  
 DR InterPro; IPR000719; Euk\_Pkinase.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003598; Ig\_C2.  
 DR InterPro; IPR001245; Tyr\_Kin.  
 DR Pfam; PF00047; Ig; 3.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR SMART; SM00219; Tyrc; 3.  
 DR SMART; SM00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;

KW Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;  
 KW Signal.  
 FT CHAIN 1 21  
 FT SIGNAL 22 819  
 FT DOMAIN 22 374  
 FT TRANSMEM 375 395  
 FT DOMAIN 396 819  
 FT DOMAIN 47 108  
 FT DOMAIN 169 235  
 FT DOMAIN 268 346  
 FT DOMAIN 125 132  
 FT DOMAIN 476 765  
 FT NP\_BIND 482 490  
 FT BINDING 512 512  
 FT ACT\_SITE 621 621  
 FT MOD\_RES 652 652  
 FT DISULFID 54 100  
 FT DISULFID 176 228  
 FT DISULFID 275 339  
 FT CARBOHYD 76 76  
 FT CARBOHYD 116 116  
 FT CARBOHYD 225 225  
 FT CARBOHYD 238 238  
 FT CARBOHYD 262 262  
 FT CARBOHYD 294 294  
 FT CARBOHYD 315 315  
 FT CARBOHYD 328 328  
 FT CONFLICT 90 90  
 SO SEQUENCE 819 AA; 91576 MW; 7E030B7AE5181DDC CRC64;

Query Match 20.3%; Score 361.5; DB 1; Length 819;  
 Best Local Similarity 32.9%; Pred. No. 4.9e-20;  
 Matches 76; Conservative 44; Mismatches 100; Indels 11; Gaps 5;

QY 61 WTKOSRTHSGSRFVLPQGLKVRQVERDAGVVCATKATNGSLVNTLVYVDIDISP 120  
 Db 65 WVRDGVQLPEN-NKRTIRIGEEYEVNDVPEDSGLACTNTSGS-ETTYSVNSDALP 122

QY 121 GKESLGPDPSSGGQEDPAS---QOMARPRETPSKMRRYIARPVGSSVRLKCVASGHP 176  
 Db 123 SAEDDDDDSDSSSEKEDNTRKPNQAVAPYWTYPKMKKLAHVAATVTKCKSGGTP 182

QY 177 RPDITWKKDQALTRPE---AAEPRKKKWTLSKLRPEDSGKYTCRYSNRAGINATY 232  
 Db 183 NPTLEMLKNGKEF-KPDHRIGGYKVRATWSTIMDSVPSDKGNVTCIYENKSGSNH 241

QY 233 KVDVIOFTRSKPVLTGTHPVNTVDFGGTTSPOCKRSDVKRYIOWLKRYE 283  
 Db 242 QLDVRSRPHRILOAGLPANKTVAGSNVEFCKVYSDPOPHIOWLKRIE 292

RESULT 11  
 FGRL\_MOUSE STANDARD; PRT; 821 AA.  
 AC P21803; 061342;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.7.1.112) (FGFR-2)  
 GN (KERATINOCYTE GROWTH FACTOR RECEPTOR).  
 GN FGFR2 OR ECT1 OR BEK.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RX MEDLINE=9228773; PubMed=1373495;  
 RA Mansukhani A., Dell'Era P., Moscattelli D., Kornbluth S.,  
 RA Hanafusa H., Basillico C.;



RT "Characterization of the murine BEK fibroblast growth factor (FGF)  
 RT receptor: activation by three members of the FGF family and  
 RT requirement for heparin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3305-3309(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A. (SHORT FORM).  
 RX MEDLINE=91095977; PubMed=1846048;  
 RA Miki T., Fleming T.P., Bottaro D.P., Rubin J.S., Ron D.,  
 RA Aaronson S.A.;  
 RA "Expression cDNA cloning of the KGF receptor by creation of a  
 RT transforming autocrine loop.";  
 RL Science 251:72-75(1991).  
 RN [3]  
 RP SEQUENCE OF 477-821 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89219016; PubMed=2468999;  
 RA Kornbluth S., Paulson K.E., Hanafusa H.;  
 RT "Novel tyrosine kinase identified by phosphotyrosine antibody  
 RT screening of cDNA libraries.";  
 RL Mol. Cell. Biol. 8:5541-5544(1988).  
 CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.  
 CC POSSESSES A HIGHER AFFINITY FOR ACIDIC THAN FOR BASIC FGF'S.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM, ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
 CC FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL, M66441; AAA37286.1; -  
 DR EMBL, M63503; AAA39377.1; -  
 DR EMBL, M23362; AAA37285.1; -  
 DR PIR, A31378; TVMSBK.  
 DR PIR, A38429; A38429.  
 DR HSSP, P11362; 1FGL.  
 DR MGD, MGI:95523; Fgfr2.  
 DR InterPro: IPR000719; Euk\_Pkinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR001245; Tyr\_Kin.  
 DR Pfam, PF00047; Ig\_3.  
 DR Pfam, PF00069; Pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
 KW Transferrase; Phosphorylation; Transmembrane; Signal;  
 KW Immunoglobulin domain; Alternative splicing.  
 FT SIGNAL 1 21  
 FT CHAIN 1 21  
 FT FT 22 821 FIBROBLAST GROWTH FACTOR RECEPTOR 2.  
 FT DOMAIN 22 377 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 378 398 POTENTIAL.  
 FT DOMAIN 399 821 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 55 114 IG-LIKE C2-TYPE DOMAIN 1.  
 FT DOMAIN 172 238 IG-LIKE C2-TYPE DOMAIN 2.  
 FT DOMAIN 271 349 IG-LIKE C2-TYPE DOMAIN 3.  
 FT DOMAIN 481 770 PROTEIN KINASE.  
 FT NP\_BIND 487 495 ATP (BY SIMILARITY).  
 FT BINDING 517 517 ATP (BY SIMILARITY).  
 FT ACT\_SITE 626 626 BY SIMILARITY.

FT MOD\_RES 657 657 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT DISULFID 62 107 POTENTIAL.  
 FT DISULFID 179 231 POTENTIAL.  
 FT DISULFID 278 342 POTENTIAL.  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPPLIC 37 37 E -> G (IN SHORT ISOFORM).  
 FT VARSPPLIC 38 152 MISSING (IN SHORT ISOFORM).  
 FT VARSPPLIC 314 361  
 FT FT  
 FT CONFLICT 169 169 AACVNTDKIEIYLRNFTFEDAGTYTLAAGSIGSRHS  
 FT CONFLICT 187 187 AMLVTLV -> HSGINSSAEVIALFNTVEMDAGEYICKVS  
 FT CONFLICT 187 187 NYIGQANOSAMLVLPKQO (IN SHORT ISOFORM).  
 FT SEQUENCE 821 AA; 91983 MW; FQDB28ADD61FA414 CRC64;  
 SO  
 Query Match 20.3%; Score 361; DB 1; Length 821;  
 Best Local Similarity 32.0%; Pred. No. 5,3e-20;  
 Matches 87; Conservative 46; Mismatches 117; Indels 22; Gaps 6;  
 QY 23 PREAPQRWRIRWGHGWRPAGPHCAAAVPPVG-----DEPLITMTXKQCRTHISGMSRF 75  
 DB 35 PEEPPRYQI-----SQPEAYVVAPEGSELQCLMDAAVISMTRKQ--VHLDPNNR 84  
 QY 76 RVL-POGLKRYQVERDAGYVCATNGFSLSVNTLVLDISPGKESIGPSSSGGQ 134  
 DB 85 TVLIGELYDQKGNTPRDSGLACTARTYDSEIWMVNTVDAISSGDEDDDSSEDEV 144  
 QY 135 EDPAQQMARPRTPQSKRRRYIARPVSSVRLKCVASGHPDPITWAKDQALT---R 191  
 DB 145 SENRSQRA-PYWTNTEKMEKRLHACPAANTVFRCPAGNPSTWRWLNKGEFEQHR 203  
 QY 192 PEAAEPRKKRWTLSTLNKLPEDSGKTCRVNSAGAINATYKVDYIQRTFRSKVGTGP 251  
 DB 204 IGGYKRWQWSLIMESVPSDKGNTCLAVENYGSINHTYHLDVVERSHRPTLDAGLP 263  
 QY 252 VNTTVDGGTTSFOCKRSDYKPVLIQMKRVE 283  
 DB 264 ANASTVVGSDVEPVCKVYSDAQPHQIKHVE 295  
 RESULT 12  
 FGR1\_HUMAN STANDARD; PRT; 822 AA.  
 ID FGR1\_HUMAN  
 AC P11362; P17049;  
 DT 01-JUL-1989 (Rel. 11. Created)  
 DT 01-MAY-1991 (Rel. 18. Last sequence update)  
 DT 20-AUG-2001 (Rel. 40. Last annotation update)  
 DE BASIC FIBROBLAST GROWTH FACTOR RECEPTOR 1 PRECURSOR (BC 2.7.1.112)  
 DE (FGR-1) (BFGF-R) (FMS-LIKE TYROSINE KINASE-2) (C-FGR).  
 GN FGR1 OR FLG OR FGFR OR FLT2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=placenta;  
 RX MEDLINE=90245600; PubMed=2159626;  
 RA Isacchi A., Bergonzoni L., Sarmientos P.;  
 RT "Complete sequence of a human receptor for acidic and basic  
 RT fibroblast growth factors.";  
 RL Nucleic Acids Res. 18:1906-1906(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Neonatal brain stem;



RX MEDLINE=90360977; PubMed=1697263;  
 RA Diome C.A., Crumley G.R., Bellot F., Kaplow J.M., Seafoss G.,  
 RA Ruta M., Bugges W.H., Jaffe M., Schlessinger J.,  
 RT "Cloning and expression of two distinct high-affinity receptors  
 RT cross-reacting with acidic and basic fibroblast growth factors.";  
 RL EMBO J. 9:2685-2692(1990).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92282615; PubMed=1317750;  
 RA Hattori Y., Odagiri H., Katoh O., Sakamoto H., Morita T.,  
 RA Shimotohno K., Tobinai K., Sugimura T., Terada M.,  
 RT "s-sam-related gene, N-sam, encodes fibroblast growth factor receptor  
 RT and is expressed in T-lymphocytic tumors.";  
 RL Cancer Res. 52:3367-3371(1992).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91126480; PubMed=1846977;  
 RA Hou J., Kan M., McKeenan K., McBride G., Adams P., McKeenan W.L.,  
 RT "Fibroblast growth factor receptors from liver vary in three  
 RT structural domains.";  
 RL Science 251:665-668(1991).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92118399; PubMed=1662973;  
 RA Klefer M.C., Baird A., George-Nascimento C., Nguyen T., Mason O.B.,  
 RA Boley L.J., Valenzuela P., Barr P.J.,  
 RT "Molecular cloning of a human basic fibroblast growth factor receptor  
 RT cDNA and expression of a biologically active extracellular domain in  
 RT a baculovirus system.";  
 RL Growth Factors 5:115-127(1991).  
 [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=90290512; PubMed=2162671;  
 RA Itoh N., Terachi T., Ohta M., Seo M.K.,  
 RT "The complete amino acid sequence of the shorter form of human basic  
 RT fibroblast growth factor receptor deduced from its cDNA.";  
 RL Biochem. Biophys. Res. Commun. 169:680-685(1990).  
 [7]  
 RP SEQUENCE OF 201-822 FROM N.A.  
 RA Ruta M., Hawk R., Ricca G., Drohan W., Zabelshansky M., Laureys G.,  
 RA Barton D.E., Francke U., Schlessinger J., Glyvol D.,  
 RT "A novel protein tyrosine kinase gene whose expression is modulated  
 RT during endothelial cell differentiation.";  
 RL Oncogene 3:9-15(1988).  
 [8]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RX MEDLINE=90355989; PubMed=2167437;  
 RA Johnson D.E., Lee P.L., Lu J., Williams L.T.,  
 RT "Inverse forms of a receptor for acidic and basic fibroblast growth  
 RT factors.";  
 RL Mol. Cell. Biol. 10:4728-4736(1990).  
 [9]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=91141499; PubMed=1847500;  
 RA Gutkind S.J., Link D.C., Katamine S., Lacal P., Miki T., Ley T.J.,  
 RA Robbins K.C.,  
 RT "A novel c-fgr exon utilized in Epstein-Barr virus-infected B  
 RT lymphocytes but not in normal monocytes.";  
 RL Mol. Cell. Biol. 11:1500-1507(1991).  
 [10]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Lung;  
 RX MEDLINE=91319400; PubMed=1650441;  
 RA Eisenann A., Ahn J.A., Graziani G., Tronick S.R., Ron D.,  
 RT "Alternative splicing generates at least five different isoforms of  
 RT the human basic-FGF receptor.";  
 RL Oncogene 6:1195-1202(1991).  
 [11]  
 RP SEQUENCE FROM N.A.  
 RA Wennerstrom S., Sandstrom C., Claesson-Welsh L.,  
 RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.

RN [12]  
 RP MUTAGENESIS OF TYR-766.  
 RX MEDLINE=92357144; PubMed=1379697;  
 RA Peters K.G., Marie J., Wilson E., Ives H.E., Escobedo J.,  
 RA del Rosario M., Mirda D., Williams L.T.,  
 RT "Point mutation of an FGF receptor abolishes phosphatidylinositol  
 RT turnover and Ca2+ flux but not mitogenesis.";  
 RL Nature 358:678-681(1992).  
 [13]  
 RP MUTAGENESIS OF TYR-766.  
 RX MEDLINE=92357145; PubMed=1379698;  
 RA Mohammadi M., Diome C.A., Li W., Lin N., Spivak T., Honegger A.M.,  
 RA Jaffe M., Schlessinger J.,  
 RT "Point mutation in FGF receptor eliminates phosphatidylinositol  
 RT hydrolysis without affecting mitogenesis.";  
 RL Nature 358:681-684(1992).  
 [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 464-762.  
 RX MEDLINE=96361355; PubMed=8752212;  
 RA Mohammadi M., Schlessinger J., Hubbard S.R.,  
 RT "Structure of the FGF receptor tyrosine kinase domain reveals a novel  
 RT autoinhibitory mechanism.";  
 RL Cell 86:577-587(1996).  
 [15]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 464-762.  
 RX MEDLINE=97284786; PubMed=9139660;  
 RA Mohammadi M., McMahon G., Sun L., Tang C., Hirth P., Yeh B.K.,  
 RA Hubbard S.R., Schlessinger J.,  
 RT "Structures of the tyrosine kinase domain of fibroblast growth factor  
 RT receptor in complex with inhibitors.";  
 RL Science 276:955-960(1997).  
 [16]  
 RP VARIANT PFEIFFER SYNDROME ARG-252.  
 RX MEDLINE=95179173; PubMed=7874169;  
 RA Muenke M., Scheil U., Hehr A., Robin N.H., Losken H.W., Schinzel A.,  
 RA Pulley L.J., Rutland P., Reardon W., Malcolm S., Winter R.M.,  
 RT "A common mutation in the fibroblast growth factor receptor 1 gene in  
 RT Pfeiffer syndrome.";  
 RL Nat. Genet. 8:269-274(1994).  
 CC -1- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR. A SHORTER  
 CC FORM OF THE RECEPTOR COULD BE A RECEPTOR FOR ACIDIC FGF (ARFGF).  
 CC -1- CATALYTIC ACTIVITY: ATP + PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: MANY FORMS OF FGFR1 ARE PRODUCED BY  
 CC ALTERNATIVE SPLICING. THE FORM SHOWN HERE IS KNOWN AS ALPHA-A1.  
 CC -1- DISEASE: DEFECTS IN FGFR1 ARE ONE OF THE CAUSES OF PFEIFFER  
 CC SYNDROME (FS) (ALSO KNOWN AS ACROCEPHALOSYNDACTYL TYPE V; ACS5);  
 CC CHARACTERIZED BY CRANIOSYNOSTOSIS (PREMATURE FUSION OF THE SKULL  
 CC SUTURES) WITH DEVIATION AND ENLARGEMENT OF THE THUMBS AND GREAT  
 CC TOES, BRACHYMESEPHALANGY, WITH PHALANGIAL ANKLYOSIS AND A VARYING  
 CC DEGREE OF SOFT TISSUE SYNDACTYL.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
 CC FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X51803; CAA36101.1; -  
 DR EMBL: X52833; CAA37015.1; -  
 DR EMBL: X66945; CAA47375.1; -  
 DR EMBL: Y00665; CAA68679.1; -  
 DR EMBL: M37722; AAA75807.1; -  
 DR EMBL: M60485; AAA35840.1; -  
 DR EMBL: M63887; AAA35958.1; -  
 DR EMBL: M34185; AAA35836.1; -  
 DR EMBL: M34186; AAA35837.1; -

DR EMBL: X57118; CAA40400.1; ALT\_TERM.  
 DR EMBL: X57119; CAA40401.1; -  
 DR EMBL: X57120; CAA40402.1; -  
 DR EMBL: X57121; CAA40403.1; -  
 DR EMBL: X57122; CAA40404.1; -  
 DR EMBL: M34641; AAA35835.1; -  
 DR EMBL: A29216; CAA01958.1; -  
 DR PIR: S11692; TVHUG.  
 DR PIR: S25420; S25420.  
 DR PIR: S26739; S26739.  
 DR PDB: 1FGK; 23-JUL-97.  
 DR PDB: 1FGI; 08-APR-98.  
 DR PDB: 1AGW; 25-MAR-98.  
 DR MIM: 136350; -  
 DR MIM: 101600; -  
 DR InterPro: IPR00719; Euk\_Pkinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_C2.  
 DR InterPro: IPR001245; Tyr\_kin.  
 DR Pfam: PF00047; Ig; 3.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; Igc2; 3.  
 DR SMART: SM00219; TyKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Receptor: Glycoprotein: Tyrosine-protein kinase; ATP-binding;  
 KW transferase; Phosphorylation; Transmembrane; Signal; 3D-structure;  
 KM immunoglobulin domain; Alternative splicing; Disease mutation.  
 FT SIGNAL 1 21 POTENTIAL.

Query Match 20.3%; Score 360.5; DB 1; Length 822;  
 Best Local Similarity 29.9%; Pred. No. 5, 8e-20;  
 Matches 87; Conservative 45; Mismatches 114; Indels 45; Gaps 8;

QY 20 RPP--PEAQRNRTKSHGRMPAGPHCAAVPEG-----DPPPLTW 61  
 DB 22 RPSPTLPEQAQP-----GAPVESEFLVHPGDLQLRCLRDVQISIN 66  
 QY 62 TKGRTHTSGWSRPRVLPGLKAYQVREDAGYVCATNGPSLSVNTLVYLDISPG 121  
 DB 67 LRGVQALAE-NRTKRTIGEVEVDSPADSGIACVTSSPS-DTTFYSVNSDLPS 124  
 QY 122 KESLGPDSSSGGQEDPA-----SQOWARPRFTOPSKMRRAVIARPVSSVRLCVAAGHP 176  
 DB 125 SEDDDDDSSSEKETDNTKPRMPVAPYVTSPEKKEKTLHAVPAKTYKFCPSGTP 184  
 QY 177 RPDITVMKDDQALTRE-----AAEPKKKWTLSKMLRPDSGKYTCRVSNRAAINATY 232  
 DB 185 NPTLRMLKNGKEF-KPDHRTIGYKVRATWSLIMDSVPSDKNGNYTCIVENEYSINHTY 243  
 QY 233 KVDVIORTSKPYLTGHPVNTVDFGCTSPCKYRSDVKPYIOWMKRNE 283  
 DB 244 QLDVERSPHRLQLAGLPAKNTVALGSSNVEFCKVYSDPHIWLKHT 294

RESULT 13  
 FGR4\_MOUSE STANDARD: PRT: 808 AA.  
 AC 003142;  
 DT 01-OCT-1994 (rel. 30, Created)  
 DT 01-OCT-1996 (rel. 34, Last sequence update)  
 DT 20-AUG-2001 (rel. 40, Last annotation update)  
 DE FIBROBLAST GROWTH FACTOR RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (FGR-4)  
 DE (PROTEIN-TYROSINE KINASE RECEPTOR MPK-11).  
 GN FGR4 OR FGR-4 OR MPK-11.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-CD-1: TISSUE-Fetal cerebellum;  
 RX MEDLINE-92146274; PubMed-1723680;  
 RA Stark K.L., McMahon J., McMahon A.P.;  
 RT "FGR-4, a new member of the fibroblast growth factor receptor  
 RT family, expressed in the definitive endoderm and skeletal muscle  
 RT lineages of the mouse."  
 RL Development 113:641-651(1992).  
 RN [2]  
 RP SEQUENCE OF 620-676 FROM N.A.  
 RC STRAIN-C57BL; TISSUE-Embryonic brain;  
 RX MEDLINE-93096484; PubMed-1281307;  
 RA Giliardi-Hebenstreit P., Nieto M.A., Fraai M., Mattei M.-G.,  
 RA Chastier A., Wilkinson D.G., Charney P.;  
 RT "An Eph-related receptor protein tyrosine kinase gene segmentally  
 RT expressed in the developing mouse hindbrain."  
 RL Oncogene 7:2499-2506(1992).  
 CC -1- FUNCTION: PUTATIVE RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.  
 CC MAY BE INVOLVED IN THE DEVELOPMENT OF SKELETAL MUSCLE CELL  
 CC LINEAGES.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE DEVELOPING GUT ENDODERM,  
 CC IN MYOTOMALLY DERIVED SKELETAL MUSCLE, THE ADRENAL CORTEX,  
 CC KIDNEY AND CONDENSING CARTILAGE. PRESENT IN ADULT LIVER,  
 CC LUNG AND KIDNEY.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
 CC FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC EMBL: X59927; CAA42551.1; -  
 DR EMBL: X57236; CAA40512.1; -  
 DR HSSP: P11362; IFGI.  
 DR MGD: MGI:95525; Fgfr4.  
 DR InterPro: IPR000719; Euk\_Pkinase.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR001245; Tyr\_kin.  
 DR Pfam: PF00047; Ig; 3.  
 DR Pfam: PF00069; pkinase; 2.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; Igc2; 3.  
 DR SMART: SM00219; TyKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
 KW transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;  
 KW Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 808  
 FT DOMAIN 19 366  
 FT DOMAIN 367 387  
 FT TRANSMEM 388 808  
 FT DOMAIN 53 98  
 FT DOMAIN 169 221  
 FT DOMAIN 268 330  
 FT DOMAIN 464 761  
 FT NP\_BIND 470 478  
 FT BINDING 509 509  
 FT ACT\_SITE 618 618  
 FT MOD\_RES 649 649  
 FT DISULFID 53 98  
 FT DISULFID 169 221  
 FT DISULFID 268 330  
 FT POTENTIAL.  
 FT FIBROBLAST GROWTH FACTOR RECEPTOR 4.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT IG-LIKE C2-TYPE DOMAIN 1.  
 FT IG-LIKE C2-TYPE DOMAIN 2.  
 FT IG-LIKE C2-TYPE DOMAIN 3.  
 FT PROTEIN KINASE.  
 FT ATP (BY SIMILARITY).  
 FT BINDING.  
 FT BY SIMILARITY.  
 FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT POTENTIAL.  
 FT POTENTIAL.  
 FT POTENTIAL.

FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 808 AA; 89775 MW; E3F30BE5E334E8B6 CRC64;

Query Match 20.2%; Score 358.5; DB 1; Length 808;  
 Best Local Similarity 33.0%; Pred. No. 8.1e-20;  
 Matches 100; Conservative 44; Mismatches 108; Indels 51; Gaps 11;

QY 37 GRWAPHCACAAVVEGDEPRLMTKDGRTIHS-----GMSRRVLPQGLKVKOVERED 91  
 DB 55 GRTERGHN-----WYKESRLASAGRYRGM-RGR-----LEIASFLPED 92  
 QY 92 AGVYCKATNGESLSVNTLVLD-----ISPKESLGPSSSGOEDPASQOMAPR 146  
 DB 93 AGRYLCIAR--GSMYVHNLTLLMDSLTISNDEDPKTLSSSSSGHYVP--QQ--APY 145  
 QY 147 FTOSKMRRIARIPVSSSVRLKCVASGHRPDITMKDOAL--TRPEAAERKKKWT 203  
 DB 146 WTHBORMEKRLHAAVPAAGNTYKFRCPACRNMPPTIHLKDGAFEGENRIGIRLRHOMWS 205  
 QY 204 LSLKRLPEDSGKYTCRVSNRAGAINATYKVDVIOFTRSKPVLGTFHPVNTTVDGEGTTS 263  
 DB 206 LYMSSVPSDRGTYTCLVENSLSGIRSYLLDVLERSHRIILDAGLPANTTAAVGSVE 265  
 QY 264 FQCKVRSDVKPVIOMLRV-----EYGAEG-----RHNSTIDVGOKFVPLPTGDVWSRPD 314  
 DB 266 LKCKVSDAQHIQMLKHVINGSSFGADGPYQVLTKTIDINISEVQVTLRVNSAEDA 325  
 QY 315 GSY 317  
 DB 326 GEY 328

RESULT 14  
 FGR2\_XENIA STANDARD; PRT; 813 AA.  
 ID FGR2\_XENIA  
 AC 003364;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE FIBROBLAST GROWTH FACTOR RECEPTOR 2 PRECURSOR (EC 2.7.1.112).  
 GN FGR2.  
 OS Xenopus laevis (African clawed frog).  
 OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Xenopodidae; Xenopus.  
 OX NCBI\_Taxid=8355;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93201992; PubMed=1284237;  
 RA Friesel R., Brown S.A.N.;  
 RT "Spatially restricted expression of fibroblast growth factor  
 receptor 2 during xenopus development.";  
 RT Development 116:1051-1058(1992).  
 RL  
 CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH  
 CC FACTORS.  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE ANTERIOR NEURAL PLATE  
 CC IN EARLY NEURULA STAGE EMBRYOS. LATER IN DEVELOPMENT, THE  
 CC PROTEIN IS ALSO EXPRESSED IN THE EYE ANLAGEN, MIDBRAIN-HINDBRAIN  
 CC BOUNDARY AND OTIC VESICLE.  
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR  
 CC FAMILY.  
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
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DR EMBL: X65943; CAA46758.1; -  
 DR PIR: S25060; S25060.  
 DR HSP; P11362; IFC1.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR001245; Tyr\_kin.  
 DR Pfam: PF00064; Ig\_3.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00219; TYRC; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Receptor: Glycoprotein; Tyrosine-protein kinase; ATP-binding;  
 KW Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;  
 KW Signal.  
 FT SIGNAL 1 14  
 FT CHAIN 15 813  
 FT DOMAIN 18 367  
 FT TRANSMEM 368 388  
 FT DOMAIN 389 813  
 FT DOMAIN 51 106  
 FT DOMAIN 163 228  
 FT DOMAIN 261 339  
 FT DOMAIN 471 760  
 FT NP\_BIND 477 485  
 FT BINDING 507 507  
 FT ACT\_SITE 616 616  
 FT MOD\_RES 647 647  
 FT CARBOHYD 79 79  
 FT CARBOHYD 115 115  
 FT CARBOHYD 231 231  
 FT CARBOHYD 255 255  
 FT CARBOHYD 287 287  
 FT CARBOHYD 308 308  
 FT CARBOHYD 321 321  
 SQ SEQUENCE 813 AA; 91340 MW; 81543656892A565 CRC64;

Query Match 18.8%; Score 334.5; DB 1; Length 813;  
 Best Local Similarity 29.5%; Pred. No. 5.3e-18;  
 Matches 87; Conservative 46; Mismatches 107; Indels 55; Gaps 10;

QY 21 PPPPAQRMRTRMSHGMPAGPCAAAVP-EGDP-----PPLMTTKDGRTHS 70  
 DB 29 PEPEPPAKYQI-----SKADVFPVLPGBDLRLCPPLADGPLVTWTKGAKLEV 77  
 QY 71 GMSRRVLPQGLKVKOVERDAGYVCKATNGFGLSNVTLVLDLSPKESLGPSS 130  
 DB 78 N-NRLIVRTYLOIKESTTRDSGLYACSVLKNHFHNAV-----EASS 121  
 QY 131 SGGEED--PASQOMAR-----PRETOSKMRRIARIPVSSSVRLKCVASGHRPDIT 181  
 DB 122 SGDEEDDDGSEEDFTNNNNIRAPYWTTEKMEKRLHAAVSAANTYKLCPPAR-EPHPSNE 180  
 QY 182 WMKDDQALT--REPAERPKKWTLSKLNRPEDSGKYTCRVSNRAGAINATYKVDVIO 238  
 DB 181 WLKNGEKQKHRIIGYKVRQHMSLWESVPSDKGYTCIVEREHSHNHTLDVIE 240  
 QY 239 FTRSKPVLGTHPVTYVDGEGTTSFOCKVSDVKPVIOMLRV-----YGAG 288  
 DB 241 RSSHRPILQAGLPANTTAAVVGDAEFYCKVSDAOPHRAWRYTEKNGSRGVG 295

RESULT 15

BFR2\_HUMAN STANDARD; PRT; 654 AA.

ID BFR2\_HUMAN STANDARD; PRT; 654 AA.

AC 001742;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (EC 2.7.1.112).

GN BFR2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=91274356; PubMed=1647213;

RA Seno M., Sasada R., Matanabe T., Ishimaru K., Igatahshi K.;

RT "Two CDNA's encoding novel human FGF receptor.";

RL Biochim. Biophys. Acta 1089:244-246(1991).

CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.

CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR FAMILY.

CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

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CC EMBL: X56191; -- NOT\_ANNOTATED\_CDS.

DR HSSP: P11362; 1FG1.

DR InterPro: IPR000719; Euk\_PKinase.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003598; Ig\_C2.

DR InterPro: IPR001245; Tyr\_Kin.

DR Pfam: PF00047; Ig\_2.

DR Pfam: PF00069; PKinase; 1.

DR PRINTS: PR00109; TYRKINASE.

DR SMART: SM00408; IGC2; 2.

DR SMART: SM00219; TYRKC; 1.

DR PROSITE: PS00109; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.

DR Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; transferase; Phosphorylation; Transmembrane; Immunoglobulin domain; Signal.

KW Signal.

FT SIGNAL 1 21

FT CHAIN 22 654

FT DOMAIN 22 263

FT TRANSMEM 264 284

FT DOMAIN 285 654

FT DOMAIN 57 123

FT DOMAIN 156 234

FT DOMAIN 367 647

FT NP\_BIND 373 381

FT BINDING 403 403

FT ACT\_SITE 512 512

FT MOD\_RES 543 543

FT CARBOHYD 113 113

FT CARBOHYD 126 126

FT CARBOHYD 150 150

FT CARBOHYD 182 182

FT CARBOHYD 203 203

FT CARBOHYD 214 214

FT CARBOHYD 235 235

SO SEQUENCE 654 AA; 73594 MW; F4954E7DC70FD233 CRC64;

Query Match 17.38; Score 307; DB 1; Length 654;

Best Local Similarity 29.38; Pred. No. 5e-16;

Matches 72; Conservative 43; Mismatches 89; Indels 42; Gaps 6;

QY 93 GVYCKATNFGSLV---NYTLVLLDISPGKESLPDSSSGQEDPASQOMARPRFTQ 149

DB 5 GRFICLVVVMATLSLARPSLSV-----EFTLEPECAPYWTN 43

QY 150 PSKMRVRVIRPVGSSVRLKCVASGHPRPITWKKDQALT--RPAAPRRKKWTLSL 206

DB 44 TEKMERLHAVPANTVKEFCPAGGNPMTMRWLKNGKEFKQEHRIIGYKVRNHWLSLM 103

QY 207 KNLPEDESGKYTCRVSRAAIAATYVQVDYIQRTSRKPVLTGHPVNTYDFGTTSFQC 266

DB 104 ESVVPSDKNTCVENEYSINHTYLDVENSPPRPILQAGLPANASTVVGDEVEVC 163

QY 267 KVSADVPVITQMLKRV---YGAEG-----RHSTIDVGQKRVLPPTGDSWRPD 314

DB 164 KVSADQPHQWIKHVKNGSKYGPDLPLYLKHSKSG---INSSNAEVLALFRVTEADA 220

QY 315 GSTLTK 320

DB 221 GEYICK 226

RESULT 16

LAR.DROME STANDARD; PRT; 2029 AA.

ID LAR.DROME STANDARD; PRT; 2029 AA.

AC P16621;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROTEIN-TYROSINE PHOSPHATASE DIAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE PHOSPHATE PHOSPHOHYDROLASE).

GN LAR.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxId=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=90046860; PubMed=2554325;

RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;

RT "A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-CANTON-S;

RX MEDLINE=96178473; PubMed=8598047;

RA Krueger N.X., van Vactor D., Wan H.I., Gelbart W.M., Goodman C.S., Saito H.;

RT "The transmembrane tyrosine phosphatase DIAR controls motor axon guidance in Drosophila.";

RL Cell 84:611-622(1996).

CC -1- FUNCTION: IT IS POSSIBLE THAT DIAR IS A CELL ADHESION RECEPTOR. IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY (PTPASE). IT CONTROLS MOTOR AXON GUIDANCE.

CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN TYROSINE + ORTHOPHOSPHATE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND PIONEER NEURONS IN THE EMBRYO.

CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

CC -1- SIMILARITY: CONTAINS 16 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.

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RT proteins provides no evidence for exon shuffling events after the  
RT separation of arthropod and chordate lineages." ;  
RT Gene 215:47-55(1998).  
RN [3]  
RP REVISIONS.  
RA Hortsch M.;  
RL submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RC STRAIN-BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos G., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodex A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jajal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Mekoylov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner C., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster." ;  
RL Science 287:2185-2195(2000).  
RN [5]  
RP SEQUENCE OF 1182-1302 FROM N.A., AND CHARACTERIZATION.  
RC TISSUE=Embryo;  
RX MEDLINE=90262720; PubMed=1693086;  
RA Hortsch M., Bieber A.J., Patel N.H., Goodman C.S.;  
RT "Differential splicing generates a nervous system-specific form of  
RT Drosophila neuroglian." ;  
RL Neuron 4:697-709(1990).  
RN [6]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 610-814.  
RX MEDLINE=94213741; PubMed=7512815;  
RA Huber A.H., Wang Y.-M.E., Bieber A.J., Bjorkman P.J.;  
RT "Crystal structure of tandem type III fibronectin domains from  
RT Drosophila neuroglian at 2.0 A." ;  
RL Neuron 12:717-731(1994).  
CC -1- FUNCTION: THE LONG ISOFORM MAY PLAY A ROLE IN NEURAL AND GLIAL  
CC CELL ADHESION IN THE DEVELOPING EMBRYO. THE SHORT ISOFORM MAY BE A  
CC MORE GENERAL CELL ADHESION MOLECULE INVOLVED IN OTHER TISSUES AND  
CC IMAGINAL DISK MORPHOGENESIS. VITAL FOR EMBRYONIC DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A  
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: LONG ISOFORM IS RESTRICTED TO SURFACE OF  
CC NEURONS AND GLIA IN THE DEVELOPING NERVOUS SYSTEM AND THE SHORT

CC ISOFORM TO OTHER NONNEURONAL TISSUES.  
CC -1- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.  
CC -----  
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CC or send an email to [license@isb.sib.ch](mailto:license@isb.sib.ch)).  
CC -----  
CC EMBL; M28231; AAA28728.2; -  
CC EMBL; AF050085; AAC28613.2; -  
CC EMBL; AF050084; AAC28613.2; JOINED.  
CC EMBL; AF050085; AAC28614.2; -  
CC EMBL; AF050084; AAC28614.2; JOINED.  
CC EMBL; AF050344; AAC28617.1; -  
CC EMBL; X76243; CA53822.1; -  
CC EMBL; X76244; CA53823.1; -  
CC PIR; A32579; A32579.  
CC PDB; 1CFB; 30-NOV-96.  
CC Flybase; FBgn0002968; Nrg.  
CC InterPro; IPR001777; FN\_III.  
CC InterPro; IPR003006; IG\_MHC.  
CC InterPro; IPR003598; IG\_C2.  
CC InterPro; IPR003600; IG\_Like.  
CC Pfam; PF00041; In3; 5.  
CC Pfam; PF00047; Ig; 6.  
CC PRINTS; PR00014; FNTYPEIII.  
CC SMART; SM00060; FN3; 5.  
CC SMART; SM00408; IGc2; 4.  
CC SMART; SM00410; IG\_Like; 2.  
CC Cell adhesion; Glycoprotein; Transmembrane; Repeat; 3d-structure;  
CC Immunoglobulin domain; Signal; Developmental protein;  
CC Alternative splicing.  
CC FT SIGNAL 1 23  
FT CHAIN 24 1302  
FT DOMAIN 24 1138  
FT TRANSMEM 1139 1154  
FT DOMAIN 1155 1302  
FT DOMAIN 53 123  
FT DOMAIN 149 224  
FT DOMAIN 262 329  
FT DOMAIN 354 422  
FT DOMAIN 447 512  
FT DOMAIN 536 606  
FT DOMAIN 629 690  
FT DOMAIN 729 792  
FT DOMAIN 832 896  
FT DOMAIN 932 997  
FT DOMAIN 1024 1098  
FT DISULFID 59 111  
FT CARBOHYD 625 706  
FT CARBOHYD 182 182  
FT CARBOHYD 198 198  
FT CARBOHYD 411 411  
FT CARBOHYD 448 448  
FT CARBOHYD 652 652  
FT CARBOHYD 683 683  
FT CARBOHYD 821 821  
FT CARBOHYD 1125 1125  
FT CARBOHYD 1224 1239  
FT VARSPLIC 1240 1302  
FT VARSPLIC 85 86  
FT CONFLICT 1282 1282  
FT CONFLICT 1302 AA; 143617 MW; 59BD9DF28675681A CRC64;  
SQ  
Query Match 12.6%; Score 225; DB 1; Length 1302;  
Best Local Similarity 24.9%; Pred. No. 1.8e-09;  
Matches 70; Conservative 43; Mismatches 98; Indels 70; Gaps 12;









RL Genomics 10:673-680(1991).  
 RP [4]  
 RP SEQUENCE OF 892-1398 FROM N.A.  
 RC TISSUE=Fibrosarcoma;  
 RX MEDLINE=92120660; PubMed=1685141;  
 RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,  
 RA Tryggvason K.,  
 RT "Cloning of human heparan sulfate proteoglycan core protein,  
 RT assignment of the gene (HSPG2) to 1p36.1->p35 and identification of  
 RT a BamHI restriction fragment length polymorphism.",  
 RL Genomics 11:389-396(1991).  
 RN [5]  
 RP SEQUENCE OF 1-21 FROM N.A.  
 RX MEDLINE=94052171; PubMed=8234307;  
 RA Cohen I.R., Graessell S., Murdoch A.D., Iozzo R.V.,  
 RT "Structural characterization of the complete human perlecan gene and  
 RT its promoter.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).  
 CC -1- FUNCTION: THIS PROTEIN IS AN INTEGRAL COMPONENT OF BASEMENT  
 CC MEMBRANES. IT IS RESPONSIBLE FOR THE FIXED NEGATIVE ELECTROSTATIC  
 CC CHARGE AND IS INVOLVED IN THE CHARGE-SELECTIVE ULTRAFILTRATION  
 CC PROPERTIES. IT INTERACTS WITH OTHER BASEMENT MEMBRANE COMPONENTS  
 CC SUCH AS LAMININ AND COLLAGEN TYPE IV AND SERVES AS AN ATTACHMENT  
 CC SUBSTRATE FOR CELLS.  
 CC -1- SUBUNIT: PURIFIED PERLECAN HAS A STRONG TENDENCY TO AGGREGATE IN  
 CC DIMERS OR SPLEATE STRUCTURES.  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.  
 CC -1- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES.  
 CC -1- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED  
 CC AND O-LINKED OLIGOSACCHARIDES.  
 CC -1- SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 10.5 LAMININ EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 LAMININ DOMAINS IV.  
 CC -1- SIMILARITY: CONTAINS 22 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 4 EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 SEA DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: X62515; CAA44373.1; -  
 CC EMBL: M85289; AAA52700.1; -  
 CC EMBL: M64283; AAA52699.1; -  
 CC EMBL: S76436; AAB21121.2; -  
 CC EMBL: I22078; -; NOT\_ANNOTATED\_CDS.  
 CC HSPG; P00740; 11XA.  
 CC MIM: 142461; -  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000742; EGF 2.  
 DR InterPro: IPR001438; EGF II.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_MHC.  
 DR InterPro: IPR002172; LDL\_recept\_A.  
 DR InterPro: IPR000034; Laminin\_B.  
 DR InterPro: IPR002049; Laminin\_EGF.  
 DR InterPro: IPR001791; Laminin\_G.  
 DR InterPro: IPR000082; SEA.  
 DR Pfam: PF00008; EGF 4.  
 DR Pfam: PF00047; Ig 22.  
 DR Pfam: PF00052; Laminin\_B 3.  
 DR Pfam: PF00053; Laminin\_EGF 8.  
 DR Pfam: PF00054; Laminin\_G 3.  
 DR Pfam: PF00057; ldl\_recept\_a 4.  
 DR Pfam: PF01390; SEA 1.  
 DR PRINTS: PRO0010; EGFBL00D.  
 DR ProDom: PD003031; Laminin\_B 3.  
 DR SMART; SM00180; EGF\_Lam; 6.  
 DR SMART; SM00001; EGF-like; 8.  
 DR SMART; SM00408; IGC2; 22.  
 DR SMART; SM00281; Lamb; 3.  
 DR SMART; SM00282; Lamb; 3.  
 DR SMART; SM00192; LDla; 4.  
 DR SMART; SM00200; SEA; 1.  
 DR PROSITE; PS00022; EGF\_1; 9.  
 DR PROSITE; PS01186; EGF\_2; 5.  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 11.  
 DR PROSITE; PS01209; LDLRA\_1; 4.  
 DR PROSITE; PS50068; LDLRA\_2; 4.  
 DR PROSITE; PS50024; SEA; 1.  
 KW Signal: Basement membrane; Proteoglycan; Repeat; Glycoprotein;  
 KW Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;  
 KW Extracellular matrix; EGF-like domain.  
 FT SIGNAL 1 21  
 FT CHAIN 22 4393  
 FT FT  
 FT DOMAIN 80 194  
 FT DOMAIN 197 236  
 FT DOMAIN 283 321  
 FT DOMAIN 323 361  
 FT DOMAIN 366 405  
 FT DOMAIN 405 506  
 FT DOMAIN 523 532  
 FT DOMAIN 533 732  
 FT DOMAIN 733 765  
 FT DOMAIN 766 815  
 FT DOMAIN 816 873  
 FT DOMAIN 881 925  
 FT DOMAIN 926 935  
 FT DOMAIN 936 1127  
 FT DOMAIN 1128 1160  
 FT DOMAIN 1161 1210  
 FT DOMAIN 1211 1267  
 FT DOMAIN 1277 1326  
 FT DOMAIN 1327 1336  
 FT DOMAIN 1337 1531  
 FT DOMAIN 1532 1564  
 FT DOMAIN 1565 1614  
 FT DOMAIN 1615 1672  
 FT DOMAIN 1679 1773  
 FT DOMAIN 1774 1867  
 FT DOMAIN 1868 1957  
 FT DOMAIN 1958 2054  
 FT DOMAIN 2054 2153  
 FT DOMAIN 2154 2246  
 FT DOMAIN 2247 2342  
 FT DOMAIN 2343 2438  
 FT DOMAIN 2439 2535  
 FT DOMAIN 2536 2631  
 FT DOMAIN 2632 2728  
 FT DOMAIN 2729 2828  
 FT DOMAIN 2829 2926  
 FT DOMAIN 2927 3024  
 FT DOMAIN 3024 3114  
 FT DOMAIN 3115 3213  
 FT DOMAIN 3214 3300  
 FT DOMAIN 3301 3401  
 FT DOMAIN 3402 3490  
 FT DOMAIN 3491 3576  
 FT DOMAIN 3577 3671  
 FT DOMAIN 3671 3847  
 FT DOMAIN 3846 3883  
 FT DOMAIN 3886 3924  
 FT DOMAIN 3924 4104  
 FT DOMAIN 4106 4143  
 FT DOMAIN 4145 4178  
 FT DOMAIN 4243 4391  
 FT SITE 65 67  
 FT SITE 71 73  
 FT SITE 76 78  
 FT SITE 4151 4153  
 FT SITE 4153

FT	SITE	4301	4303	(POTENTIAL). MEDIATES MOTOR NEURON ATTACHMENT (POTENTIAL).
FT	DISULFID	199	212	BY SIMILARITY.
FT	DISULFID	206	225	BY SIMILARITY.
FT	DISULFID	219	234	BY SIMILARITY.
FT	DISULFID	285	297	BY SIMILARITY.
FT	DISULFID	292	310	BY SIMILARITY.
FT	DISULFID	304	319	BY SIMILARITY.
FT	DISULFID	325	337	BY SIMILARITY.
FT	DISULFID	332	350	BY SIMILARITY.
FT	DISULFID	344	359	BY SIMILARITY.
FT	DISULFID	368	381	BY SIMILARITY.
FT	DISULFID	375	394	BY SIMILARITY.
Query Match		12.5%	Score 222.5;	DB 1; Length 4393;
Best Local Similarity		28.4%	Pred. No. 1,1e-08;	
Matches	63; Conservative	33;	Mismatches	75; Indels 51; Gaps 8;
QY	53	GDPEPLMTMTKDGRTIHSGMSRFRVLPGC--LKVKOVEREDAGVYVCATNGFGLSVNY	110	
Db	3516	GDPKQVYMWSKGHLRPG-----IVGSGGVVRIAHVELADAGXRCRTATNAAGTQSHV	3570	
QY	111	TLVVLDDISPGKESLGPPSSSGGQEDPASQOMARPRFTQPSMKRRVILARPSSVRLKC	170	
Db	3571	LLLV-----QALPOLISMPQEV-----VPAGSAVAPFC	3598	
QY	171	VASGPRPDITMMKDDALTRPEAEPPKKKWTLSLKNLRPDSCKYTCGVSNRGAJNA	230	
Db	3599	IASGPTPDIDISKIDGSL-----PPDSRIENMLMLPSPQPDAGTYCTATNRQSKVNA	3654	
QY	231	TYKVDVIGRTRSKPVLTGTN---PVNTTVDFGCTTSFQCKV	268	
Db	3655	FAHLQVPERV--VPYFTQTPTYSFLPLTIKD--AVRKKEPIKI	3692	
RESULT	21			
FGRL	DROME	STANDARD:	PRT;	730 AA.
AC	007407:			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	FIBROBLAST GROWTH FACTOR RECEPTOR HOMOLOG 1 PRECURSOR (EC 2.7.1.112)			
DE	(HEARTLESS PROTEIN).			
GN	FRL OR HTL OR DFRL.			
SS	Drosophila melanogaster (Fruit fly).			
SS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
SS	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OC	NCBI_Taxid=7227;			
RA	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RA	MEDLINE=94156202; PubMed=8112607;			
RA	Ito M., Matsui T., Taniguchi T., Chihara K.;			
RT	"Alternative splicing generates two distinct transcripts for the			
RT	drosophila melanogaster fibroblast growth factor receptor homolog."			
RL	Gene 139:215-218(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CANTON-S;			
RX	MEDLINE=93321617; PubMed=8330538;			
RA	Shishido E., Higashijima S.-I., Emori Y., Saigo K.;			
RT	"Two FGF receptor homologues in early embryos."			
RL	mesodermal primordium in early embryos."			
CC	Development 117:751-761(1993).			
CC	-1- FUNCTION: MAY BE REQUIRED FOR PATTERNING OF MUSCLE PRECURSOR			
CC	CELLS. WOULD THUS APPEAR ESSENTIAL FOR GENERATION OF MESODERMAL			
CC	AND ENDODERMAL LAYERS, INVASIONS OF VARIOUS TYPES OF CELLS,			
CC	AND CNS FORMATION.			
CC	-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN			
CC	TYROSINE PHOSPHATE.			

CC	-1	SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.	
CC	-1	TISSUE SPECIFICITY: MESODERM.	
CC	-1	DEVELOPMENTAL STAGE: EMBRYOGENESIS.	
CC	-1	SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR FAMILY.	
CC	-1	SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.	
CC	-1	CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-16 IS THE INITIATOR.	
CC			
DR	EMBL: D14976;	BAA03616.1; -	
DR	EMBL: D14977;	BAA03617.1; -	
DR	EMBL: X74030;	CAA52189.1; -	
DR	HSSP: P11362;	1FG1.	
DR	FLYbase:	FBgn0010389; htl.	
DR	InterPro: IPR000719;	Euk_pkinase.	
DR	InterPro: IPR003006;	Ig_MHC.	
DR	InterPro: IPR003598;	Ig_C2.	
DR	InterPro: IPR003600;	Ig_1Ike.	
DR	InterPro: IPR001245;	Tyr_kin.	
DR	Pfam: PF00047;	Ig_1.	
DR	Pfam: PF00069;	kinase; 1.	
DR	PRINTS: PR00109;	TYRKINASE.	
DR	SMART: SM00408;	IGC2; 1.	
DR	SMART: SM00410;	IG_1Ike; 1.	
DR	SMART: SM00219;	TyKc; 1.	
DR	PROSITE: PS00107;	PROTEIN_KINASE_ATP; 1.	
DR	PROSITE: PS00109;	PROTEIN_KINASE_TYR; 1.	
DR	PROSITE: PS50011;	PROTEIN_KINASE_DOM; 1.	
KW	Receptor;	Glycoprotein; Tyrosine-protein kinase; ATP-binding;	
KW	transferase;	phosphorylation; transmembrane; immunoglobulin domain;	
KW	Signal.		
FT	CHAIN	1	34
FT			POTENTIAL FIBROBLAST GROWTH FACTOR RECEPTOR HOMOLOG 1.
FT	DOMAIN	35	730
FT	TRANSMEM	35	309
FT	DOMAIN	310	333
FT	DOMAIN	334	730
FT	DOMAIN	118	181
FT	DOMAIN	213	279
FT	DOMAIN	417	693
FT	NP_BIND	423	431
FT	BINDING	444	444
FT	ACT_SITE	557	557
FT	MOD_RES	588	588
FT	DISULFID	125	174
FT	DISULFID	220	272
FT	CARBOHYD	60	60
FT	CARBOHYD	70	70
FT	CARBOHYD	96	96
FT	CARBOHYD	134	134
FT	CARBOHYD	140	140
FT	CARBOHYD	171	171
FT	CARBOHYD	207	207
FT	CARBOHYD	213	213
FT	CARBOHYD	242	242
FT	CARBOHYD	246	246
FT	CARBOHYD	282	282
FT	CONFLICT	77	77
FT	CONFLICT	167	167
FT	CONFLICT	218	218
FT	CONFLICT	237	237
FT	CONFLICT	359	359
FT	CONFLICT	431	431
FT	CONFLICT	505	505
FT	CONFLICT	508	509
FT	CONFLICT	563	563



AC PA3146;  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 40, Last annotation update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).  
GN DCC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RX MEDLINE=95011532; PubMed=7926722;  
RA Hedrick L., Cho K.R., Fearon E.R., Wu T.-C., Kinzler K.W.,  
RA Vogelstein B.;  
RT "The DCC gene product in cellular differentiation and colorectal  
RT tumorigenesis.";  
RT Genes Dev. 8:1174-1183(1994).  
RN [2]  
RX MEDLINE=90100559; PubMed=2294591;  
RA Fearon E.R., Cho K.R., Ngirto J.M., Kern S.E., Simons J.W.,  
RA Ruppert J.M., Hamilton S.R., Preisinger A.C., Thomas G., Kinzler K.W.,  
RA Vogelstein B.;  
RT "Identification of a chromosome 18q gene that is altered in  
RT colorectal cancers.";  
RT Science 247:49-56(1990).  
RN [3]  
RX MEDLINE=91121517; PubMed=1991322;  
RA Ngirto J.M., Cho K.R., Fearon E.R., Kern S.E., Ruppert J.M.,  
RA Oliner J.D., Kinzler K.W., Vogelstein B.;  
RT "Scrambled exons.";  
RT Cell 64:607-613(1991).  
RN [4]  
RX GENE STRUCTURE, AND VARIANTS CARCINOMA HIS-1375.  
RX MEDLINE=94245241; PubMed=8188295;  
RA Cho K.R., Oliner J.D., Simons J.W., Hedrick L., Fearon E.R.,  
RA Preisinger A.C., Hedge P., Silverman G.A., Vogelstein B.;  
RT "The DCC gene: structural analysis and mutations in colorectal  
RT carcinomas.";  
RT Genomics 19:525-531(1994).  
RN [5]  
RX VARIANT CARCINOMA THR-168, AND VARIANT GLY-201.  
RX MEDLINE=94243823; PubMed=8187090;  
RA Miyake S., Nagai K., Yoshino K., Ota M., Endo M., Yusa Y.;  
RT "Point mutations and allelic deletion of tumor suppressor gene DCC in  
RT human esophageal squamous cell carcinomas and their relation to  
RT metastasis.";  
RT Cancer Res. 54:3007-3010(1994).  
RN [6]  
RX C-1 FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.  
RX C-1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
RX C-1 TISSUE SPECIFICITY: FOUND IN AXONS OF THE CENTRAL AND PERIPHERAL  
RX C-1 NERVOUS SYSTEM AND IN DIFFERENTIATED CELL TYPES OF THE INTESTINE.  
RX C-1 DISEASE: COLORECTAL TUMORS THAT LOST THEIR CAPACITY TO  
RX C-1 DIFFERENTIATE INTO MUCUS PRODUCING CELLS UNIFORMLY LACK DCC  
RX C-1 EXPRESSION. INACTIVATION OF DCC DUE TO ALLELIC DELETION AND/OR  
RX C-1 POINT MUTATIONS MAY CAUSE BOTH LYMPHATIC AND HEMATOGENOUS  
RX C-1 METASTASIS OF COLORECTAL SQUAMOUS CELL CARCINOMAS.  
RX C-1 SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
RX C-1 SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; X76132; CA53735.1; -  
CC EMBL; M32286; AAA52174.1; -  
CC EMBL; M32286; AAA52174.1; -

DR EMBL; M32286; AAA52175.1; ALT\_SEQ.  
DR EMBL; M32290; AAA52176.1; -  
DR EMBL; M63696; AAA52177.1; -  
DR EMBL; M63700; AAA52178.1; -  
DR EMBL; M63702; AAA52179.1; -  
DR EMBL; M63718; AAA52180.1; -  
DR EMBL; M63698; AAA52181.1; -  
DR PIR; A54100; A54100.  
DR PIR; A40098; A40098.  
DR PIR; A38442; A38442.  
DR HSSP; P56276; ITLK.  
DR MIM; 120470; -  
DR InterPro; IPR001777; FN\_III.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003598; IG\_C2.  
DR InterPro; IPR003600; IG\_1like.  
DR Pfam; PF00041; fn3; 6.  
DR Pfam; PF00047; Ig; 4.  
DR PRINTS; PR00014; FNTPEIII.  
DR SMART; SM00060; FN3; 6.  
DR SMART; SM00408; IGc2; 3.  
DR SMART; SM00410; IG\_1like; 2.  
DR GlycoProtein; Immunoglobulin domain; Transmembrane; Signal;  
DR Anti-Oncogene; Disease mutation; Polymorphism.  
KW SIGNAL  
FT CHAIN 1 25  
FT 26 1447  
FT 26 1097  
FT 1098 1122  
FT TRANSSEM 1123 1447  
FT DOMAIN 1123 1447  
FT DOMAIN 54 124  
FT DOMAIN 154 219  
FT DOMAIN 254 317  
FT DOMAIN 345 407  
FT DOMAIN 426 522  
FT DOMAIN 525 618  
FT DOMAIN 619 716  
FT DOMAIN 722 816  
FT DOMAIN 840 940  
FT DOMAIN 941 1042  
FT DISULFID 61 117  
FT DISULFID 161 212  
FT DISULFID 261 310  
FT DISULFID 352 400  
FT CARBOHYD 94 94  
FT CARBOHYD 299 299  
FT CARBOHYD 318 318  
FT CARBOHYD 478 478  
FT CARBOHYD 628 628  
FT CARBOHYD 702 702  
FT VARIANT 168 168  
FT VARIANT 201 201  
FT VARIANT 1375 1375  
FT VARIANT 138 138  
FT CONFLICT 233 329  
FT CONFLICT 421 421  
SO SEQUENCE 1447 AA; 158456 MW; 4A861276ED0471F CRC64;  
  
Query Match 11.68; Score 207; DB 1; Length 1447;  
Best Local Similarity 26.78; Pred. No. 4.66-08;  
Matches 66; Conservative 34; Mismatches 87; Indels 60; Gaps 9;  
  
QY 51 VEGDPPPLTMTKGR--TIHSGMSRFVLPDQ--LKVQVREDAAGVYVCKATNGFGLS 107  
DB 163 VIGEMPTTHQKNQDLPFGDSRYVLPDQSLRDLPGDGLTRCSARN----- 216  
QY 108 VNYTLVLDLSPKESIGPSSGQEDPASQOQWARRFTOPSKMRRV--IARP----- 161  
DB 217 -----PASSRTGNE-----AEVRIISDPDLHQLVFLQPSNVV 250

QY 162 --VGSSVRLKCVASGHPRPDITMKNDDQALTRPEAEPRKKWT-----LSLKNLRPED 213  
 DB 251 AIEGRDAVLECCVSGYPPSFTWLKGE-----EYQLRSKRYSLGSGNLSNVTTDD 304  
 QY 214 SGKYTCRVSNRAGAINATYKVDVIOKTRSKVLTGTHPVNTVDFGTTSFQCKVRSDDK 273  
 DB 305 SGMYTCVVTYNNENISASAEILTVL-----VPPWFLNHPNSNLVAYESMDIEFECVYSGRPV 359  
 QY 274 PVIOMLK 280  
 DB 360 PTVNMMK 366

RESULT 24  
 DCC\_MOUSE STANDARD; PRT; 1447 AA.  
 ID P70211;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DT TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.  
 CC DCC.  
 CC Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBL\_TaxID=10090;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC STRAIN-BALB/C; TISSUE-Brain;  
 CC MEDLINE=96112625; PubMed=8570174;  
 CC Cooper H.M., Ames P., Britto J., Gad J., Wilks A.F.;  
 CC "Cloning of the mouse homologue of the deleted in colorectal cancer  
 CC gene (mDCC) and its expression in the developing mouse embryo.";  
 CC Oncogene 11:2243-2254(1995).  
 CC [2]  
 CC REVISIONS.  
 CC STRAIN-BALB/C; TISSUE-Brain;  
 CC Cooper H.M.;  
 CC Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: IMPLICATED AS A TUMOR SUPPRESSOR GENE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: TWO FORMS OF THE PROTEIN ARE PRODUCED FROM  
 CC THE SAME GENE BY THE USE OF ALTERNATIVE INITIATION SITES. A THIRD  
 CC FORM WHICH IS EXPRESSED ONLY IN THE EMBRYO IS PRODUCED BY  
 CC ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED AT HIGH LEVELS IN THE  
 CC DEVELOPING BRAIN AND NEURAL TUBE. IN ADULT, HIGHLY EXPRESSED IN  
 CC BRAIN WITH VERY LOW LEVELS FOUND IN TESTIS, HEART AND THYMUS.  
 CC -1- DEVELOPMENTAL STAGE: LOW LEVELS IN EARLY GESTATION. HIGHEST LEVELS  
 CC EXPRESSED DURING MID GESTATION. LEVELS DECREASE IN LATE GESTATION  
 CC AND REMAIN AT THIS LEVEL IN THE ADULT.  
 CC -1- SIMILARITY: CONTAINS 4 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: X85788; CAA59786.1; -  
 CC HSSP: P56276; ITK.  
 CC MGD: MGI:94869; DCC.  
 CC InterPro: IPR001777; FN.III.  
 CC InterPro: IPR003006; IG.MHC.  
 CC InterPro: IPR003598; IG.C2.  
 CC InterPro: IPR003600; IG.Like.  
 CC Pfam: PF00041; tns3; 6.  
 CC Pfam: PF00047; tns3; 4.  
 CC PRINTS: PR00014; FNTPYELII.  
 CC SMART: SM00060; FN3; 6.

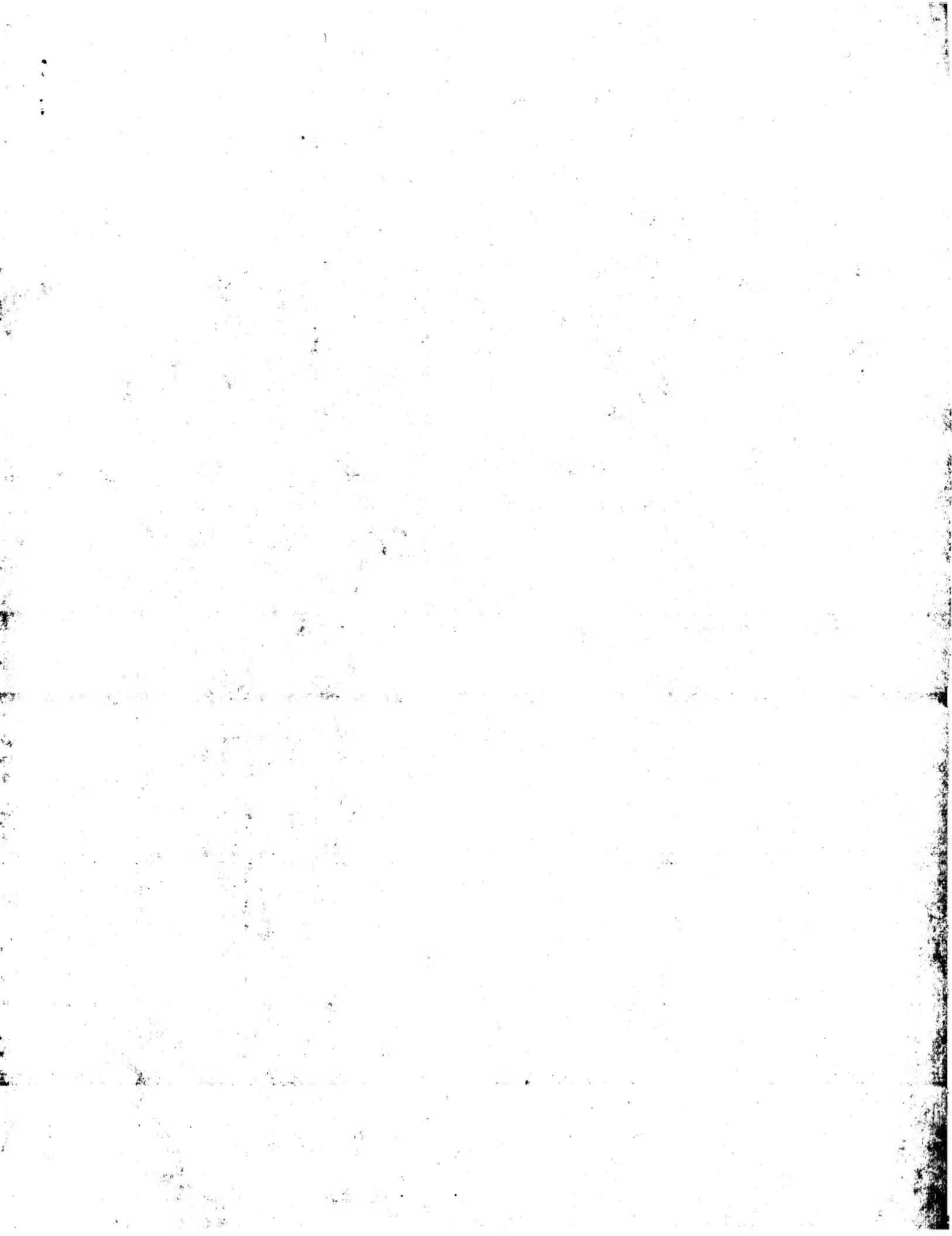
DR SMART: SM00408; IGc2; 3.  
 DR SMART: SM00410; IG\_Like; 2.  
 KW Glycoprotein; Immunoglobulin domain; Transmembrane; signal;  
 KW Anti-oncogene; Alternative Initiation; Alternative splicing.  
 FT SIGNAL 1 25  
 FT CHAIN 26 1447  
 FT TUMOR SUPPRESSOR PROTEIN DCC, LONG  
 FT ISOFORM.  
 FT TUMOR SUPPRESSOR PROTEIN DCC, SHORT  
 FT ISOFORM.  
 FT FOR SHORT ISOFORM.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT IG-LIKE C2-TYPE DOMAIN 1.  
 FT IG-LIKE C2-TYPE DOMAIN 2.  
 FT IG-LIKE C2-TYPE DOMAIN 3.  
 FT IG-LIKE C2-TYPE DOMAIN 4.  
 FT FIBRONECTIN TYPE-III 1.  
 FT FIBRONECTIN TYPE-III 2.  
 FT FIBRONECTIN TYPE-III 3.  
 FT FIBRONECTIN TYPE-III 4.  
 FT FIBRONECTIN TYPE-III 5.  
 FT FIBRONECTIN TYPE-III 6.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT DISULFID 261 310  
 FT DISULFID 352 400  
 FT CARBOHYD 60 60  
 FT CARBOHYD 94 94  
 FT CARBOHYD 299 299  
 FT CARBOHYD 318 318  
 FT CARBOHYD 478 478  
 FT CARBOHYD 628 628  
 FT CARBOHYD 702 702  
 FT CARBOHYD 819 838  
 FT VARSPLIC 838  
 FT MISSING (IN EMBRYONIC ISOFORM).  
 FT SEQUENCE 1447 AA; 158298 MW; 0D1F1097C22D5B9F CRC64;

Query Match 11.6%; Score 207; DB 1; Length 1447;  
 Best Local Similarity 26.3%; Pred. No. 4, 6e-08;  
 Matches 65; Conservative 36; Mismatches 86; Indels 60; Gaps 9;

QY 51 VEGDPPPLTMTWKDGRTH--SGMSRFRVLPQ--LTKOVERDAGVYCKATNGSGSIS 107  
 DB 163 VIEGPMPTIHWKQNDLNPDPDSVVVLPSCALQISLQGDSDSVYCSARN----- 216  
 QY 108 VNTTLVVDLDSIGKSLPDDSSGGQEDPASQMARPRFTOPSKRRRY--IARP----- 161  
 DB 217 -----PASIRTGEN-----AEVRILSDPGIHRQLYFLORPSNYI 250  
 QY 162 --VGSSVRLKCVASGHPRPDITMKNDDQALTRPEAEPRKKWT-----LSLKNLRPED 213  
 DB 251 AIEGRDAVLECCVSGYPPSFTWLKGE-----EYQLRSKRYSLGSGNLSNVTTDD 304  
 QY 214 SGKYTCRVSNRAGAINATYKVDVIOKTRSKVLTGTHPVNTVDFGTTSFQCKVRSDDK 273  
 DB 305 SGMYTCVVTYNNENISASAEILTVL-----VPPWFLNHPNSNLVAYESMDIEFECVYSGRPV 359  
 QY 274 PVIOMLK 280  
 DB 360 PTVNMMK 366

RESULT 25  
 AXOL\_RAT STANDARD; PRT; 1040 AA.  
 ID AXOL\_RAT  
 AC P22063;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE CONTACTIN 2 PRECURSOR (AXONIN-1) (AXONAL GLYCOPROTEIN TAG-1)  
 DE (TRANSIENT AXONAL GLYCOPROTEIN 1) (TAG-1).  
 GN CNTN2 OR TAX1.









```
85 213 12.0 1059 22 AAU00825 Human immune respo
86 213 12.0 1059 22 AAB80261 Human PRO335 prote
87 213 12.0 1119 20 AAY08114 Human PRO326 prote
88 213 12.0 1119 21 AAY70674 Human PRO326 prote
89 213 12.0 1119 22 AAY12347 Human PRO326 polyp
90 213 12.0 1119 22 AAU00827 Human immune respo
91 213 12.0 1119 22 AAB80263 Human PRO326 polyp
92 213 12.0 1119 22 AAB48162 Human PRO326 polyp
93 212.5 11.9 739 22 AAB62398 Human MBSP2 polype
94 210.5 11.8 791 20 AAY08096 Murine glial cell
95 210.5 11.8 825 20 AAY08115 Murine glial cell
96 210.5 11.8 1091 18 AAM41641 Sequence used in d
97 210.5 11.8 1091 20 AAY08099 Murine glial cell
98 210.5 11.8 1091 20 AAY08010 Mouse Lig-1 protei
99 210.5 11.8 1091 21 AAY97833 Murine Lig-1 prote
100 208.5 11.7 932 22 AAE05252 Mouse Nope (neighb
```

## ALIGNMENTS

## RESULT 1

ID AAB19116 standard; Protein; 322 AA.

AC AAB19116;

DT 19-FEB-2001 (first entry)

DE Homologue of polypeptide from lymph node stromal cells of fsn -/- mice.

KW Lymph node stromal cell; fsn -/- mice; inflammatory disorder;

KW immune system disorder; cancer; viral infection; HIV infection;

KW blood vessel growth; tumour necrosis factor disorder; arthritis;

KW inflammatory bowel disease; fibroblast growth factor-mediated disorder;

KW cardiac failure.

KW Homo sapiens.

KW WO200058463-A1.

PD 05-OCT-2000.

PF 18-FEB-2000; 2000WO-NZ00015.

PR 25-MAR-1999; 99US-0276268.

PR 26-AUG-1999; 99US-0383586.

PR (GENE-) GENESIS RES &amp; DEV CORP LTD.

PR Strachan L, Sleeman M, Abernethy N, Onrust R, Kumble KD;

PR Murison JG;

PR MPI: 2000-664924/64.

PR N-PSDB; AAA96726.

PR Polypeptide expressed in mammalian fsn -/- lymph node stromal cells,

PR useful for modulating growth of blood cells, for treating inflammatory

PR and tumour necrosis factor-mediated disorders, cancer and viral

PR disorders

PS Claim 1; Page 53-54; 75pp; English.

PS The present sequence represents a homologue of a polypeptide sequence

PS which is isolated from lymph node stromal cells of fsn -/- mice. The

PS CC polynucleotides and their polypeptides are useful for treating an

PS CC inflammatory disorder, disorder of immune system and cancer selected

PS CC from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a

PS CC viral disorder, in particular HIV infection and for modulating the

PS CC growth of blood vessels. The polypeptides are useful for treating a

PS CC tumour necrosis factor (TNF) mediated disorder, such as those selected

PS CC from arthritis, inflammatory bowel disease and cardiac failure and a

PS CC fibroblast growth factor-mediated disorder. It is also useful in assays

to determine biological activity, to raise antibodies, to isolate corresponding ligands or receptors, to quantify levels of protein or cognate corresponding ligand or receptors, as anti-inflammatory agents, and in compositions for the treatment of skin, connective tissue and CC immune system diseases. The polynucleotide is useful as marker for CC tissue, as a chromosome marker or tags in the identification of a CC genetic disorder.

SQ Sequence 322 AA;

Query Match

Best Local Similarity 100.0%; Score 1779; DB 21; Length 322;

Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRAPCCCSCRCRCGSHRPPPEAPORRRTWSHGRMPAGHCAAPVEGDPPLTM 60

DB 1 RRAPCCCSCRCRCGSHRPPPEAPORRRTWSHGRMPAGHCAAPVEGDPPLTM 60

QY 61 WTKDGRTHSGSRFRVLPGLKVKOVERDAGVYCKATNGRGSLSVNTLVLDISP 120

DB 61 WTKDGRTHSGSRFRVLPGLKVKOVERDAGVYCKATNGRGSLSVNTLVLDISP 120

QY 121 GKESLGPDSSSSGQEDPASQOMARPRFTOPSKRRRRVIRAPVSSVRLKCVASGHRPDI 180

DB 121 GKESLGPDSSSSGQEDPASQOMARPRFTOPSKRRRRVIRAPVSSVRLKCVASGHRPDI 180

QY 181 TWMKDQALTRPPAAPRRKKKTLKLNLPEDSGYTCRVSRACAINATKYVDVIQRT 240

DB 181 TWMKDQALTRPPAAPRRKKKTLKLNLPEDSGYTCRVSRACAINATKYVDVIQRT 240

QY 241 RSKPVLTHGHPVNTWTFDGGTTSFOCKVRSQVSPVOWLKRVEYEGRHNSRTIDVGQK 300

DB 241 RSKPVLTHGHPVNTWTFDGGTTSFOCKVRSQVSPVOWLKRVEYEGRHNSRTIDVGQK 300

QY 301 FVVLPTGVDWSPRPGSYLNKPL 322

DB 301 FVVLPTGVDWSPRPGSYLNKPL 322

RESULT 2

AAB24066 standard; Protein; 504 AA.

AC AAB24066;

DT 29-JAN-2001 (first entry)

DE Human PRO943 protein sequence SEQ ID NO:29.

KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;

KW proliferation; tumorigenesis; identification; cancer; cytostatic;

KW neurotropic; neuroprotective; anti-inflammatory; immunosuppressive;

KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;

KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;

KW hypothalamic disorder; glandular disorder; macropagal disorder;

KW epithelial disorder; stromal disorder; blastocoele disorder;

KW inflammatory disorder; immunologic disorder.

OS Homo sapiens.

PN WO200053755-A2.

PD 14-SEP-2000.

PF 06-JAN-2000; 2000WO-US00376.

PR 08-MAR-1999; 99WO-US005028.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 26-OUL-1999; 99US-0145698.

PR 30-NOV-1999; 99WO-US28313.



FT Peptide /label= antigenic  
FT 483..496  
XX /label= antigenic  
PN WO200024756-A1.  
XX 04-MAY-2000.  
PD 17-JUN-1999; 99MO-US13620.  
XX 23-OCT-1998; 98US-0105465.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Ruben SM, Young PE;  
XX WPI: 2000-387035/33.  
DR N-PSDB; AAA28842.  
XX  
XX Nucleic acids encoding fibroblast growth factor-5 useful for the  
PT prevention, diagnosis and treatment of conditions associated with  
PT tissue repair and aberrant cell functions, e.g. cell survival and  
PT proliferation  
XX  
XX Claim 11: Fig 1A-C; 182pp; English.

CC This is the fibroblast growth factor receptor protein, FGFR-5. The  
CC FGFR-5 protein and DNA may be used in the prevention, treatment and  
CC diagnosis of diseases or conditions associated with inappropriate FGFR-5  
CC expression and activity. For example, the nucleic acids (and vectors  
CC containing them) and the FGFR-5 polypeptide may be used to treat  
CC disorders associated with increased or decreased cell survival (such as  
CC cancers (e.g. leukemia, colonic cancer, testicular cancer and follicular  
CC lymphomas), autoimmune disorders (e.g. multiple sclerosis and Crohn's  
CC disease) viral infections (e.g. herpes viruses), inflammation, graft  
CC versus host disease, acute and chronic graft rejection, ischemic injuries  
CC and atherosclerosis), activation, secretion, migration, differentiation  
CC and proliferation, diseases associated with defects in wound healing,  
CC mucositis, defects of angiogenesis, immune dysfunction, endocrine  
CC dysfunction and insulin secretion disorders. Anti-FGFR-5 antibodies may  
CC also be used as diagnostic agents for detecting the presence of FGFR-5  
CC polypeptides in samples.

Sequence 504 AA:

Query Match 81.4%; Score 1448; DB 21; Length 504;  
Best Local Similarity 99.6%; Pred. No. 7.9e-98;  
Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

NY 50 PVEGDPEPLTMTKDGRTTHSGMSRRFVLPQGLKQVEREDAGVYVCKATNGFSGLSVN 109  
DB 52 PVEGDPEPLTMTKDGRTTHSGMSRRFVLPQGLKQVEREDAGVYVCKATNGFSGLSVN 111  
QY 110 YTLVVDLDTSPGKESLGPSSSGGODPAQQAARPRFTQPSKRRRVARAPGVSSYRLK 109  
DB 112 YTLVVDLDTSPGKESLGPSSSGGODPAQQAARPRFTQPSKRRRVARAPGVSSYRLK 111  
QY 170 CVASGHPRPDITMMKDDQALTRPEAAERKKKWTLSLKNRPDSGKYTRVSNRGAIN 229  
DB 172 CVASGHPRPDITMMKDDQALTRPEAAERKKKWTLSLKNRPDSGKYTRVSNRGAIN 231  
QY 230 ATYKVDVIOKTRSKPVLGTGHPVNTVDFGGTTSFOCKVRSVDPYTWLKLREYGAEGR 289  
DB 232 atykvdvigttrskpvlgtgphpvntlvdfggttsfgckvrsdvkpylqwlkreygaegr 291  
QY 290 HNSTIDVGOKFVYLPRTGDVMSRPDSYLNKPL 322  
DB 292 hnstidvggkfvlylptgdvmsrpdsgsylnkpl 324

RESULT 4  
AAV66656

ID AAV66656 standard; protein; 504 AA.  
XX AAV66656;  
AC AAV66656;  
XX 05-APR-2000 (first entry)  
DT  
XX  
DE Membrane-bound protein PR0943.  
XX  
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.  
XX  
OS Homo sapiens.  
XX  
PN WO963088-A2.  
PD 09-DEC-1999.  
XX  
XX 02-JUN-1999; 99MO-US12252.  
XX  
XX 02-JUN-1998; 98US-0087607.  
PR 02-JUN-1998; 98US-0087609.  
XX 02-JUN-1998; 98US-0087759.  
PR 03-JUN-1998; 98US-0087827.  
XX 04-JUN-1998; 98US-0088021.  
PR 04-JUN-1998; 98US-0088025.  
XX 04-JUN-1998; 98US-0088028.  
PR 04-JUN-1998; 98US-0088029.  
XX 04-JUN-1998; 98US-0088030.  
PR 04-JUN-1998; 98US-0088033.  
XX 04-JUN-1998; 98US-0088326.  
PR 05-JUN-1998; 98US-0088167.  
XX 05-JUN-1998; 98US-0088202.  
PR 05-JUN-1998; 98US-0088212.  
XX 05-JUN-1998; 98US-0088217.  
PR 09-JUN-1998; 98US-0088655.  
XX 10-JUN-1998; 98US-0088722.  
PR 10-JUN-1998; 98US-0088730.  
XX 10-JUN-1998; 98US-0088734.  
PR 10-JUN-1998; 98US-0088738.  
XX 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
XX 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
XX 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
XX 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
XX 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
XX 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
XX 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
XX 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
XX 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
XX 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
XX 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
XX 17-JUN-1998; 98US-0089601.  
PR 18-JUN-1998; 98US-0089603.  
XX 18-JUN-1998; 98US-0089607.  
PR 18-JUN-1998; 98US-0089608.  
XX 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
XX 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
XX 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
XX 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.



DE Human PRO943 (UNQ480) protein sequence SEQ ID NO:119.  
 XX  
 XX Human: secreted and transmembrane protein; PRO: cytosolic;  
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;  
 KW diagnostic assay.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200073454-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 XX 30-MAR-2000; 2000MO-US08439.  
 XX  
 XX 02-JUN-1999; 99MO-US12252.  
 XX 23-JUN-1999; 99US-0141037.  
 XX 07-JUL-1999; 99US-0143048.  
 XX 20-JUL-1999; 99US-0144758.  
 XX 26-JUL-1999; 99US-0145698.  
 XX 28-JUL-1999; 99US-0146222.  
 XX 17-AUG-1999; 99US-0149396.  
 XX 15-SEP-1999; 99MO-US21090.  
 XX 08-OCT-1999; 99MO-US21547.  
 XX 30-NOV-1999; 99US-0158663.  
 XX 01-DEC-1999; 99MO-US28301.  
 XX 16-DEC-1999; 99MO-US30095.  
 XX 20-DEC-1999; 99MO-US30911.  
 XX 05-JAN-2000; 2000MO-US00219.  
 XX 06-JAN-2000; 2000MO-US00376.  
 XX 11-FEB-2000; 2000MO-US03565.  
 XX 18-FEB-2000; 2000MO-US04341.  
 XX 22-FEB-2000; 2000MO-US04414.  
 XX 24-FEB-2000; 2000MO-US04914.  
 XX 02-MAR-2000; 2000MO-US05004.  
 XX 15-MAR-2000; 2000MO-US05841.  
 XX 20-MAR-2000; 2000MO-US07377.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Fong S, Gether H, Gertlisen ME, Goddard A, Godowski PJ,  
 PI Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoletti NF,  
 PI Roy MA, Stewart JA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;  
 XX  
 DR WPI: 2001-032160/04.  
 DR N-PSDB; AAF44130.  
 XX  
 PT PRO polynucleotides used to produce polypeptides used to target  
 PT bioactive molecules such as toxins, radiolabels or antibodies, to  
 PT specific cells, to cause targeted cell death -  
 XX  
 PS Claim 12; Fig 70; 935pp; English.  
 XX  
 CC The present invention describes human secreted and transmembrane PRO  
 CC proteins. The PRO proteins have cytosolic activity. The PRO proteins  
 CC can be used for targeted delivery of bioactive molecules, such as  
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide  
 CC sequences, and their fragments, can be used as hybridisation probes, in  
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA  
 CC and DNA. They may also be used to produce transgenic animals which are  
 CC used to develop and screen therapeutically useful reagents. The PRO  
 CC nucleotide and protein sequence can be used for tissue typing and in  
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.  
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes  
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and  
 CC AAB5514 to AAB5300 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SO Sequence 504 AA:

Query Match 81.4%; Score 1448; DB 22; Length 504;  
 Best Local Similarity 99.6%; Pred. No. 7.9e-98;  
 Matches 212; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 50 PVEGDPPPLTMMTKDGRRTISGMSRFRVLPOGLKVKOVEREDAGVYCKATNGFGSLVN 109  
 DB 52 pvegdppplcmwtkdgrlthsgwsrfrvlpqglkvkqveredagvyckatngfslvn 111  
 QY 110 YTLVVLDDISPGKESLGPDSSSGQEDPASQOMARPRPTOPSKMRRVIAAPGVSSVRLK 169  
 DB 112 ytlvvlddispgkeslgpdsssgqedpasqoqarprftgskmrrvriarpygssvrlk 171  
 QY 170 CVASGHRPRDITMMKDDOALTRPEAAEPRKKMTLSIKNLRPDSGCTTCRVSNRGAIN 229  
 DB 172 cvasghrprdtlmmkddqaltrpeaaepkktwlsiknlrpdsgcttcrvsnr gain 231  
 QY 230 ATTKVDVLTQTRSKPVLGTGHPVNTTVDFGTTSPQCKRSDVKPVIOMLRYEYGAEGR 289  
 DB 232 attkvdvltqtrskpvlgtghpnttvdftgtsfgckvrsdvkpvilqwikreygaegr 291  
 QY 290 HNSTIDVGGKFPVLPFGDWSRPDSYLNKPL 322  
 DB 292 hnstldvggkfpvlptgdwsrpdsgsylnkpl 324  
 RESULT 6  
 ID AAB66264 standard; Protein; 504 AA.  
 XX  
 AC AAB66264;  
 XX  
 DT 05-APR-2001 (first entry)  
 XX  
 DE Human MANGO 003 SEQ ID NO: 5.  
 XX  
 XX Membrane associated protein; secreted protein; human; mouse; rat;  
 KW INTERCEPT 340; MANGO 003; MANGO 347; TANGO 272; TANGO 295; TANGO 354;  
 KW TANGO 378; skeletal disorder; cardiovascular disorder; renal disorder;  
 KW haematopoietic disorder; neural disorder; hepatic disorder;  
 KW neoplastic disease.  
 XX  
 OS Homo sapiens.  
 OS  
 OS  
 PN WO200100673-A1.  
 XX  
 PD 04-JAN-2001.  
 XX  
 PF 29-JUN-2000; 2000MO-US18198.  
 XX  
 PR 30-JUN-1999; 99US-0345464.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Barnes TM, Fraser CC, Wrighton N, Myers P, Busfield SJ, Sharp JD;  
 PI WPI: 2001-050128/06.  
 DR N-PSDB; AAF27781.  
 XX  
 PT Isolated secreted or transmembrane proteins are used for diagnosis and  
 PT treatment of neoplastic and haematopoietic disorders e.g. T cell  
 PT disorders, cancer and tumours -  
 XX  
 PS Claim 9; Page 216-217; 294pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences for a  
 CC number of membrane associated and secreted proteins from human, mouse and  
 CC rat. The proteins are designated INTERCEPT 340, MANGO 003, MANGO 347,  
 CC TANGO 272, TANGO 295, TANGO 254 and TANGO 378. The proteins are all  
 CC involved in signal transduction and the sequences can be used in the  
 CC treatment of cardiovascular, renal, hepatic, neural, neoplastic, skeletal  
 CC and haematopoietic disorders.

SQ Sequence 504 AA;

Query Match 81.4%; Score 1448; DB 22; Length 504;  
 Best Local Similarity 99.6%; Pred. No. 7.9e-98;  
 Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 PVEGDPPPLTMMTKDGRTHSGMSRFRVLPQGLKVKYQVEREDAGYVCKATNGFGLSVN 109  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 52 pvegdpppltmwtkdgrthhsgwsfrvlpqglkvkyqveredagyyvckatngfglsvn 111  
 QY 110 YTLVVLDDISPGKESLGPDSGGQEDPASQOMARPRFTOPSKMRRYIARPVGSSVRLK 169  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 112 ytlvvladdispgkeslpgdssgggedpasqgwarprftgskmrryiarpvgsavrlk 171  
 QY 170 CVASGHRPPDITWMKDDQALTRPEAEPRKKRWLTLKLNLRPEDSGKYTCRVSNRGAIN 229  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 172 cvasghrppdltwmkddqaltrpeaeprkkwllslknlrpedsgkytcrvsnragaIn 231  
 QY 230 ATYKVDVIGRTSRKPVLTGTHPVNTVDFGCTSPQCKVRSVDVPIQWLKRVEXGAGGR 289  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 232 atykvvdvigrtrskpvlgtchpntlvdfgctsfqckvrsdvkpvqlwlvkveygaeqr 291  
 QY 290 HNSTIDVGQKFFVLPTEGDVWSRPPGSLYLNKPL 322  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 292 hnstidvggkfvlptegdvwsrpdgslYlnkll 324

## RESULT 7

AAM38643 ID AAM38643 standard; Protein: 608 AA.

AC AAM38643;

DF 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 1788.

XX Human; noctropic; immunosuppressant; cyostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.

OS Homo sapiens.

PN MO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US34263.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

PA (HSE-) HXSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX WPT: 2001-442253/47.  
 DR N-PSDB; AA157799.  
 XX Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -

XX Example 3: SEQ ID NO 1788; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with noctropic,  
 CC immunosuppressant and cyostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.

SQ Sequence 608 AA;

Query Match 81.4%; Score 1448; DB 22; Length 608;  
 Best Local Similarity 99.6%; Pred. No. 9.6e-98;  
 Matches 272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 PVEGDPPPLTMMTKDGRTHSGMSRFRVLPQGLKVKYQVEREDAGYVCKATNGFGLSVN 109  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 39 pvegdpppltmwtkdgrthhsgwsfrvlpqglkvkyqveredagyyvckatngfglsvn 98  
 QY 110 YTLVVLDDISPGKESLGPDSGGQEDPASQOMARPRFTOPSKMRRYIARPVGSSVRLK 169  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 99 ytlvvladdispgkeslpgdssgggedpasqgwarprftgskmrryiarpvgsavrlk 158  
 QY 170 CVASGHRPPDITWMKDDQALTRPEAEPRKKRWLTLKLNLRPEDSGKYTCRVSNRGAIN 229  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 159 cvasghrppdltwmkddqaltrpeaeprkkwllslknlrpedsgkytcrvsnragaIn 218  
 QY 230 ATYKVDVIGRTSRKPVLTGTHPVNTVDFGCTSPQCKVRSVDVPIQWLKRVEXGAGGR 289  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 219 atykvvdvigrtrskpvlgtchpntlvdfgctsfqckvrsdvkpvqlwlvkveygaeqr 278  
 QY 290 HNSTIDVGQKFFVLPTEGDVWSRPPGSLYLNKPL 322  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 279 hnstidvggkfvlptegdvwsrpdgslYlnkll 311

## RESULT 8

AAB19114 ID AAB19114 standard; Protein: 529 AA.

AC AAB19114;

DF 19-FEB-2001 (first entry)

DE Polypeptide isolated from lymph node stromal cells of fsn -/- mice.

XX Lymph node stromal cell; fsn -/- mice; inflammatory disorder;  
 KW immune system disorder; cancer; viral infection; HIV infection;  
 KW blood vessel growth; tumour necrosis factor disorder; arthritis;  
 KW inflammatory bowel disease; fibroblast growth factor-mediated disorder;  
 KW cardiac failure.

OS Mus sp.

PN MO200058463-A1.

PD 05-OCT-2000.

PF 18-FEB-2000; 2000WO-NZ00015.

PR 25-MAR-1999; 99US-0276268.

PR 26-AUG-1999; 99US-0383586.  
 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 XX Strachan L, Sleeman M, Abernethy N, Onrust R, Kumble KD;  
 PI Morrison JG;  
 XX WPI: 2000-664924/64.  
 DR N-PSDB; AAA96724.  
 XX  
 PT Polypeptide expressed in mammalian fsn -/- lymph node stromal cells,  
 PT useful for modulating growth of blood cells, for treating inflammatory  
 PT and tumor necrosis factor-mediated disorders, cancer and viral  
 PT disorders  
 XX  
 PS Claim 1; Page 51-52; 75pp; English.  
 XX  
 CC The present sequence represents a polypeptide sequence which is  
 CC isolated from lymph node stromal cells of fsn -/- mice. The  
 CC polynucleotides and their polypeptides are useful for treating an  
 CC inflammatory disorder, disorder of immune system and cancer selected  
 CC from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a  
 CC viral disorder, in particular HIV infection and for modulating the  
 CC growth of blood vessels. The polypeptides are useful for treating a  
 CC tumor necrosis factor (TNF) mediated disorder, such as those selected  
 CC from arthritis, inflammatory bowel disease and cardiac failure and a  
 CC fibroblast growth factor-mediated disorder. It is also useful in assays  
 CC to determine biological activity, to raise antibodies, to isolate  
 CC corresponding ligands or receptors, to quantify levels of protein or  
 CC cognate corresponding ligand or receptors, as anti-inflammatory agents,  
 CC and in compositions for the treatment of skin, connective tissue and  
 CC immune system diseases. The polynucleotide is useful as marker for  
 CC tissue, as a chromosome marker or tags in the identification of a  
 CC genetic disorder.  
 XX  
 SQ Sequence 529 AA:  
 77.1%; Score 1371; DB 21; Length 529;  
 Best Local Similarity 93.4%; Pred. No. 3.4e-92;  
 Matches 255; Conservative 8; Mismatches 10; Indels 0; Gaps 0;  
 Query Match  
 Db 50 PVSQDPPPLMTWKDGRTHISGSRPRVLPQGLKVKOVEREDAGVYCKATNGEGLSVN 109  
 48 PVEGDDPPLMTWKDGRTHISGSRPRVLPQGLKVKOVEREDAGVYCKATNGEGLSVN 107  
 QY 110 YTLVLVDDISPGKESLGPDSGGEDPASQOMARPRFTOPSKMRRVIRAPVSSVRLK 169  
 108 YTLIMDDISPGKESLGPDSGGEDPASQOMARPRFTOPSKMRRVIRAPVSSVRLK 167  
 Db 170 CVASGHRPDIYWKDDQALTRPEAAEPRKKWTLISLKNLPEDSGKYTCRVSNRGA 229  
 168 CVASGHRPDIYWKDDQALTRPEAAEPRKKWTLISLKNLPEDSGKYTCRVSNRGA 227  
 Db 230 ARKKVUVIORTRSKPVLTGHPVNTVDFGCTTSFOCKVRSVDKPVYIOMLKREYGAEGR 269  
 228 ARKKVUVIORTRSKPVLTGHPVNTVDFGCTTSFOCKVRSVDKPVYIOMLKREYGAEGR 267  
 QY 290 HNSTIDVGOKFVLPPTGVDWSPRDSYLNRPL 322  
 288 HNSTIDVGOKFVLPPTGVDWSPRDSYLNRPL 320  
 Db  
 RESULT 9  
 AAB19115  
 ID AAB19115 standard: Protein; 439 AA.  
 XX  
 AC AAB19115;  
 XX  
 DT 19-FEB-2001 (first entry)  
 XX  
 DE Polypeptide isolated from lymph node stromal cells of fsn -/- mice.  
 XX

KW Lymph node stromal cell; fsn -/- mice; inflammatory disorder;  
 KW immune system disorder; cancer; viral disorder; HIV infection;  
 KW blood vessel growth; tumor necrosis factor disorder; arthritis;  
 KW inflammatory bowel disease; fibroblast growth factor-mediated disorder;  
 KW cardiac failure.  
 XX  
 XX Mus sp.  
 XX  
 XX W0200058463-A1.  
 XX  
 XX 05-OCT-2000.  
 XX  
 XX 18-FEB-2000; 2000WC-NZ00015.  
 XX  
 XX 25-MAR-1999; 99US-0276268.  
 XX 26-AUG-1999; 99US-0383586.  
 XX  
 XX (GENE-) GENESIS RES & DEV CORP LTD.  
 XX Strachan L, Sleeman M, Abernethy N, Onrust R, Kumble KD;  
 PI Morrison JG;  
 XX WPI: 2000-664924/64.  
 DR N-PSDB; AAA96725.  
 XX  
 PT Polypeptide expressed in mammalian fsn -/- lymph node stromal cells,  
 PT useful for modulating growth of blood cells, for treating inflammatory  
 PT and tumor necrosis factor-mediated disorders, cancer and viral  
 PT disorders  
 XX  
 PS Claim 1; Page 52-53; 75pp; English.  
 XX  
 CC The present sequence represents a polypeptide sequence which is  
 CC isolated from lymph node stromal cells of fsn -/- mice. The  
 CC polynucleotides and their polypeptides are useful for treating an  
 CC inflammatory disorder, disorder of immune system and cancer selected  
 CC from epithelial, lymphoid, myeloid, stromal and neuronal cancers, a  
 CC viral disorder, in particular HIV infection and for modulating the  
 CC growth of blood vessels. The polypeptides are useful for treating a  
 CC tumor necrosis factor (TNF) mediated disorder, such as those selected  
 CC from arthritis, inflammatory bowel disease and cardiac failure and a  
 CC fibroblast growth factor-mediated disorder. It is also useful in assays  
 CC to determine biological activity, to raise antibodies, to isolate  
 CC corresponding ligands or receptors, to quantify levels of protein or  
 CC cognate corresponding ligand or receptors, as anti-inflammatory agents,  
 CC and in compositions for the treatment of skin, connective tissue and  
 CC immune system diseases. The polynucleotide is useful as marker for  
 CC tissue, as a chromosome marker or tags in the identification of a  
 CC genetic disorder.  
 XX  
 SQ Sequence 439 AA:  
 57.8%; Score 1029; DB 21; Length 439;  
 Best Local Similarity 93.7%; Pred. No. 2.4e-67;  
 Matches 194; Conservative 4; Mismatches 9; Indels 0; Gaps 0;  
 Query Match  
 Db 23 ddispgkesspgpssgggedpasqwarprftqpskmrrvlarvsgsvrlkcvasgh 82  
 176 PRPDIYWKDDQALTRPEAAEPRKKWTLISLKNLPEDSGKYTCRVSNRGA1NATYKVD 235  
 83 PRPDIYWKDDQALTRPEAAEPRKKWTLISLKNLPEDSGKYTCRVSNRGA1NATYKVD 142  
 Db 236 VIORTRSKPVLTGHPVNTVDFGCTTSFOCKVRSVDKPVYIOMLKREYGAEGRHNSTD 295  
 143 VIORTRSKPVLTGHPVNTVDFGCTTSFOCKVRSVDKPVYIOMLKREYGAEGRHNSTD 202  
 QY 296 VGGOKFVLPPTGVDWSPRDSYLNRPL 322  
 203 VGGOKFVLPPTGVDWSPRDSYLNRPL 229  
 Db



RESULT 10  
AAM25511  
ID AAM25511 standard; Protein: 365 AA.  
XX  
AC AAM25511;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human protein sequence SEQ ID NO:1026.  
XX  
KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;  
KW antibacterial; endocrine; cardiast; central nervous system; virucide;  
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;  
KW antiaggregant; haemostatic; vulnery; antilucer; osteopathic; eczema;  
KW dermatological; antiallergic; antiallumatic; antidiabetic; cytosstatic;  
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
KW neurological disorder.  
XX  
OS Homo sapiens.  
XX  
PN MO200153455-A2.  
XX  
PD 26-JUL-2001.  
XX  
PE 22-DEC-2000; 2000WO-US35017.  
XX  
PF 23-DEC-1999; 99US-0471275.  
XX  
PR 21-JAN-2000; 2000US-0488725.  
XX  
PR 25-APR-2000; 2000US-0552317.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI: 2001-457603/49.  
DR N-PSDB: AAH99452.  
XX  
PT Isolated human polynucleotides encoding polypeptides, useful for the  
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
XX  
PS Claim 20; Page 210; 1217pp: English.  
XX  
CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
CC AAM25963. The proteins can have activities based on the tissues and  
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;  
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiast;  
CC central nervous system; virucide; anti-HIV; fungicide; antilucer;  
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;  
CC antilucer; osteopathic; dermatological; antiallergic; antiasthmatic;  
CC antidiabetic; cytosstatic; neuroprotective; antidepressant; nootropic;  
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
CC encoding them can be used in gene therapy, antisense therapy and vaccine  
CC production. The proteins and polynucleotides are useful for screening for  
CC agonists or antagonists of a protein and for the treatment and diagnosis  
CC of disorders associated with the activity of a protein e.g. inflammation,  
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
CC neurological disorders.  
XX

SQ Sequence 365 AA:  
Query Match 57.3%; Score 1019; DB 22; Length 365;  
Best Local Similarity 99.5%; Pred. No. 1e-66;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 130 SSGGQEDPASOOWARPRTOPSKMRRVIAIPVGSVLLKCAVSGHPDPDMMKDDAL 189  
DB 5 ssggqedpasqwarprltqpskmrrvlaipvgsavllkcaasphprpdlmddqal 64  
QY 190 TRPEAAEPKRRKMTLSLKNLRPEDSGKYTCRVSNAGA INATYKVDVIOFTRSKPEVLATGT 249  
DB 65 trpeaeprkkkwtlslnlripedsqkytcrrsnagalnaykvdvigrtskplvltgt 124  
QY 250 HPVNTTVDPGGTSFQCKVRSDVKPVIOMLKREYGAEGRNSTIDVGQKRVVLPBGDV 309  
DB 125 hpvnttvdgftsfgckvrsdvkpvlgwlrkveygaegrnstdvggqkfvlpbgdv 184  
QY 310 MSRPDGSYLNRPL 322  
DB 185 wsrpdgsylnrpl 197  
RESULT 11  
AAM40429  
ID AAM40429 standard; Protein: 371 AA.  
XX  
AC AAM40429;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 5360.  
XX  
KW Human; nootropic; immunosuppressant; cytosstatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia.  
XX  
OS Homo sapiens.  
XX  
PN MO200153312-A1.  
XX  
PD 26-JUL-2001.  
XX  
PE 26-DEC-2000; 2000WO-US34263.  
XX  
PF 21-JAN-2000; 2000US-0488725.  
XX  
PR 25-APR-2000; 2000US-0552317.  
XX  
PR 09-JUL-2000; 2000US-0598042.  
XX  
PR 19-JUL-2000; 2000US-0620312.  
XX  
PR 03-AUG-2000; 2000US-0653450.  
XX  
PR 14-SEP-2000; 2000US-0662191.  
XX  
PR 19-OCT-2000; 2000US-0693036.  
XX  
PR 29-NOV-2000; 2000US-0727344.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao Qa, Zhou P, Goodrich R, Drmanac RT;  
XX  
DR WPI: 2001-442253/47.  
DR N-PSDB: AAI59585.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -  
XX  
PS Example 2; SEQ ID NO 5360; 10078pp: English.  
XX  
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and

DR	N-PSDB; AAF16334.
PT	Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer -
PT	
P5	Claim 11; Page 2183; 238bp; English.
XX	
CC	AAI5566 to AAI6505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302
CC	The prostate cancer antigens can have neuroprotective, cytosolic,
CC	cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
CC	nephrotoxic, antiinfective, gynaecological and antibacterial activities
CC	and can be used in gene therapy. The prostate cancer antigen
CC	polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive,
CC	gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC	AAB57303 represent sequences used in the exemplification of the present invention.
CC	
SQ	Sequence 101 AA;
OY	Query Match 29.7%; Score 529; DB 21; Length 101;
OY	Best Local Similarity 99.0%; Pred. No. 1.3e-31;
Matches	99; Conservative 1; Mismatches 0; Indels 0; Gaps 0
D5	171 VASGHPDDITMMKDDOALTRPEAERPRKKKWTLISLNLRPEDSGKYTCRVNRAGAINA 230       1 vasghprdditmmkddqaltrpeaaeprrkkkwtlislknlrpedsgkytcrvnraina 60
OY	231 TYKVDTIGTFRSKPVLGTGHVNTFYDPFGTSSFOCKVRS 270       61 tykvdtigtrskpvlgtghvntfydpgtcsfgckvrt 100
RESULT 13	
ID	AAU02951
AC	AAU02951 standard; Protein; 389 AA.
XX	
XX	AAU02951;
DT	
XX	
DE	12-SEP-2001 (first entry)
XX	
KW	Angiotensin converting enzyme (ACEV) splice variant protein #51.
KW	Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW	granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW	platelet-derived endothelial cell growth factor; cardiovascular disease;
KW	cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1c;
KW	vessolative intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW	myocardial infarction; coronary arterial thrombosis; renal disease;
KW	diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW	multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW	noncarcinoidic pulmonary granulomatous disease; endothelial abnormality;
XX	
OS	Homo sapiens.
PN	WO200136632-A2.
XX	
PD	25-MAY-2001.
XX	
PF	17-NOV-2000; 2000MO-IL00766.
PR	17-NOV-1999; 99TL-0132978.
PR	10-DEC-1999; 99TL-0133455.
XX	
XA	(COMP-) COMPEND LTD.
XX	



```
QY 246 LSTHPVNTTVDGTTSPQCKVRSQDKPVYIOMLKRVEYGAEGRHNSITIDVGOKFY-VL 304
DB 255 Lqgdlpanqtavlgsvdfeihckvysdaqphlqwlkhnev-----ngskvypdglpyvtl 309
QY 305 PT 306
DB 310 kt 311

RESULT 15
AAR15264
ID AAR15264 standard; Protein; 355 AA.
AC AAR15264;
DE 18-FEB-1992 (first entry)
EX Extracellular domain of FGF receptor.
KW Plasmid PTB1290; fibroblast growth factor; cancer.
OS Homo sapiens.
PN WO9117183-A.
PD 14-NOV-1991.
PE 25-APR-1991; 91WO-JP00557.
PR 28-DEC-1990; 90JP-0415801.
PR 27-APR-1990; 90JP-0113146.
PR 31-JUL-1990; 90JP-0204438.
PR 14-SEP-1990; 90JP-0245256.
XX (TAKE ) TAKEDA CHEMICAL IND KK.
XX Igarashi K, Senoo M, Watanabe T;
XX WPI; 1991-353723/48.
XX N-PSDB; AAQ14864.
XX New muten(s) of proteins - with fibroblast growth factor
XX receptor activity, useful for treating multiple endocrine
XX neoplasia, prostatic hypertrophy, used for diagnosis
XX
XX Claim 5; Fig 12; 88pp; English.
XX
CC A cDNA library prepared from human cancer cell line Kato III mRNA
CC was screened with an oligonucleotide corresponding to amino acids
CC 529-541 of chicken basic FGF receptor. Positive clones were inserted
CC into pUC118/119 and the recombinant plasmids were used to transform
CC E.coli MV1184. Single-stranded DNA was prepared from two of the
CC transformants for use as a template in site-directed mutagenesis.
CC Eventually the sequence corresponding to the extracellular domain
CC was cloned into plasmid pET3c under the control of the T7 promoter.
CC This amino acid sequence was deduced from the nucleotide sequence
CC of the insert from plasmid pTB1390. The transformant E.coli
CC MM294(DE3)/plyss, pTB1290 (FERM BP-3217) is claimed. See also AAQ14845.
XX
XX Sequence 355 AA;

Query Match 21.1%; Score 375.5; DB 12; Length 355;
Best Local Similarity 29.9%; Pred. No. 8e-20;
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;
```

```
DB 65 tvligelyldkgsatprdsqlyactaartvdsctwfmvntdaisgdd-----edtdtda 120
QY 135 EDPASQ---OWAPRPTQDSKMRRIARVGVSSVRLKCVASGHPDPITWMKDQALR- 190
DB 121 edfvsensnmkrapywtntekmekrlhavpaantvfrpcaggnpmtmwlkngefbq 180
QY 191 --RPEAAEPKKKKWTLSTLNKLRPDSGKTYCRNSNAGAINATYKXVDYQRTSKRVLVG 248
DB 181 ehriqgykvrngdhwslmesvpsdkgnylcvvenegyslnhtlyldversphrpilga 240
QY 249 THPVTNTVDGTTSPQCKVRSQDKPVYIOMLKRVE-----YGAEG-----RHNSITIDV 296
DB 241 glpanastvrgdvtefvckvysdaqphlqwlkhnevkngekygpdglpylkhkhsq---i 297
QY 297 GGOKEFVLPFGDVSKRPDGSYLNK 320
DB 298 nssnaevlalfvteadageylok 321

RESULT 16
AAR15267
ID AAR15267 standard; Protein; 643 AA.
AC AAR15267;
DE 18-FEB-1992 (first entry)
EX Clone PTB1229-encoded protein with FGF receptor activity.
KW Human; fibroblast growth factor; cancer.
OS Homo sapiens.
PN WO9117183-A.
PD 14-NOV-1991.
PE 25-APR-1991; 91WO-JP00557.
PR 28-DEC-1990; 90JP-0415801.
PR 27-APR-1990; 90JP-0113146.
PR 31-JUL-1990; 90JP-0204438.
PR 14-SEP-1990; 90JP-0245256.
XX (TAKE ) TAKEDA CHEMICAL IND KK.
XX Igarashi K, Senoo M, Watanabe T;
XX WPI; 1991-353723/48.
XX N-PSDB; AAQ14849.
XX New muten(s) of proteins - with fibroblast growth factor
XX receptor activity, useful for treating multiple endocrine
XX neoplasia, prostatic hypertrophy, used for diagnosis
XX
XX Example 2; Fig 4; 88pp; English.
XX
CC A cDNA library prepared from human cancer cell line Kato III mRNA
CC was screened with an oligonucleotide corresponding to amino acids
CC 529-541 of chicken basic FGF receptor. Three positive clones were
CC obtained and were cloned into pUC118/119 to give pTB1227, pTB1228
CC and pTB1229. The longest clone was in pTB1229. The amino acid
CC sequence was deduced from the insert sequence.
XX
XX Sequence 643 AA;

Query Match 21.1%; Score 375.5; DB 12; Length 643;
Best Local Similarity 29.9%; Pred. No. 1.5e-19;
Matches 97; Conservative 55; Mismatches 129; Indels 43; Gaps 10;
```

Db 35 peepptkyqf-----sgpevyvaapgesleivrcllkdaavistwkdg--vhlgnmr 84  
 QY 76 RVL-PQGLKQYVEREDAGYVCKATNGPGLSNVTLYVLDLSPKESLGPSSSGGQ 134  
 Db 85 tllgeylqikgaptsglyactastvdselwfmvntvdaisgdd-----edddga 140  
 QY 135 EDPAQ---QWAPRFTQPSKRRRVIARPVSSVRLKCVASGHPRDITWMDQALF- 190  
 Db 141 edfvsensnkrpypvntekmekrlhvaantvktfcpcagngpmptumtvlknqkefkq 200  
 QY 191 --RPEAEPKKKWTLSLKLRLPEDSKGYTCRVSNRAGAINATYKVVDIORTSKPVLTG 248  
 Db 201 ehrtgykfvnqnqhwslimesvpsdkgnlcvvneygslnhtyhldiversphrpilga 260  
 QY 249 THPVNTVDSGTTSPQCKYRSDVKPYIOMLKRYE-----YGAGS-----RHNSTIDV 296  
 Db 261 glpenastvvgdvctekkyvsdaqphlqwlkvkknsgkyypgdlpylklvknsg---1 317  
 QY 297 GGQKFVVLPTGVDWSRPDSGLNKK 320  
 Db 318 nsnnaevlalfvnteadageyick 341

## RESULT 17

AAR39647  
 ID AAR39647 standard; protein: 816 AA.

XX AAR39647;

DT 14-JAN-1994 (first entry)

DE Human fibroblast growth factor receptor.

XX soluble; FGF-R: fibroblast growth factor receptor; tumour therapy;  
 KW immunoglobulin-like domain; tyrosine kinase activity; hyperplasia;  
 KW psoriasis; Herpes Simplex Virus; HSV.

XX Homo sapiens.

XX Location/Qualifiers

FT Cleavage-site 21..22 /note= "putative signal peptidase site"

FT Domain 55..101 /label= Ig-like\_domain\_1

FT Domain 179..231 /label= Ig-like\_domain-2

FT Domain 278..341 /label= Ig-like\_domain-3

FT Region 126..133 /label= AR

FT /note= "acidic amino acid rich region"

FT Misc-difference 137..143 /note= "the sequence EEKKEKE in Seq.ID.No.1 is shown as EEKE in Fig. 2"

FT Domain 372..392 /label= transmembrane

FT Domain 475..575 /label= Tyrosine\_kinase\_domain

FT /note= "first part of split TK domain"

FT /label= Tyrosine\_kinase\_domain

FT /note= "second part of split TK domain"

XX US5229501-A.

XX 20-JUL-1993.

XX 11-JAN-1991: 91US-0640029.

XX 11-JAN-1991: 91US-0640029.

XX (CHIR ) CHIRON CORP.

PI Barr PJ, Kelfer MC, Valenzuela PDR;  
 XX WPI; 1993-242535/30.  
 DR New recombinant human fibroblast growth factor receptor - is  
 PT useful in treatment of hyperplasia(s), tumours and herpes simplex  
 PT infection  
 XX Claim 1: Fig 2 and Columns 13-18; 21pp; English.  
 PS The invention covers both the full-length FGF-receptor and its  
 CC soluble form (i.e. truncated by deletion of the C-terminal portion  
 CC beginning at the transmembrane domain). The FGF receptor is defined  
 CC as having the sequence in Columns 13-18 and Fig 2. These sequences  
 CC differ slightly as indicated by the "Misc.difference" in the  
 CC Features table. The receptor can be used to detect FGF or to inhibit  
 CC FGF activity. Specifically, the soluble form of the receptor can  
 CC inhibit FGF-dependent tumour growth, angiogenesis, psoriasis,  
 CC excessive scar formation and hyperplasias and can be used to treat  
 CC Herpes simplex virus infections.  
 CC Sequence 816 AA:

Query Match 21.0%; Score 373; DB 14; Length 816;  
 Best Local Similarity 30.1%; Pred. No. 3.1e-19;  
 Matches 89; Conservative 46; Mismatches 115; Indels 46; Gaps 8;

QY 20 RPPP--PEAPQWRTKMSHGMRPAGPCAAAPVEG-----DPPPLTW 61  
 Db 22 rpsplclpegqpw-----gapvevesflvhpqdlqlrcrlrdvgslnw 66  
 QY 62 TKDGRTHSGMSRRFVLPOGLKQYVEREDAGYVCKATNGPGLSNVTLYVLDLSPG 121  
 Db 67 lrdvqlaes-ntrltgeevqdsvpadsqlyactvsspsg-dtlytsvnvdaips 124  
 QY 122 KESLGPSSSGGGE-----DPASQWAPRFTQPSKRRRVIARPVSSVRLKCVASGH 175  
 Db 125 seddddddsssekekekdntknpvayvtspekmekklhvaapakvktfcpsst 184  
 QY 176 PRPDITWMDQALTRPE---AAEPKKKWTLSLKLRLPEDSKGYTCRVSNRAGAINAT 231  
 Db 185 pncflrwlknqkef-kpdrtygykvatwsilmdsvpsdkgnlcvvneygslnht 243  
 QY 232 YKVVDIORTSKPVLTGTHPVNTVDSGTTSPQCKYRSDVKPYIOMLKRYEAGAE 287  
 Db 244 yqldversphrpilqaglpanktvalgsnvelmckvysdpqphlqwlkhlwsgsk 299

## RESULT 18

AAR15268  
 ID AAR15268 standard; protein: 769 AA.

XX AAR15268;

DT 18-FEB-1992 (first entry)

DE Clone pFBI284-encoded complete FGF receptor.

XX Human; fibroblast growth factor; cancer.

XX Homo sapiens.

XX WO9117183-A.

XX 14-NOV-1991.

XX 25-APR-1991: 91WO-JP00557.

XX 28-DEC-1990: 90JP-0415801.

XX 27-APR-1990: 90JP-0113146.

XX 31-JUL-1990: 90JP-0204438.

XX 14-SEP-1990: 90JP-0245256.





XX Novel fusion protein constructs comprise a fibroblast growth factor (FGF) receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin (Ig) I segment fused to a heterologous oligomerization domain that comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4 region, or light chain of an immunoglobulin molecule, or a peptide with a leucine zipper motif. The Ig I segment is not necessary for binding of acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the affinity for aFGF and heparin, protects the core of the molecule from proteolysis, and abrogates the heparin requirement for aFGF binding. The new fusion polypeptides are better FGF inhibitors than FGF-R monomer proteins. The FGF-R-Ig Fc fusion dimers are active as FGF antagonists at subnanomolar concentrations and were 20-fold more potent than the FGF-R monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-mediated disorders, such as tumorigenesis (e.g. bladder, breast, lung, rectal, testis and cervical tumors), neovascularization (e.g. diabetic retinopathy, neovascular glaucoma), wound healing and corneal scarring) and hyper-proliferation of vascular smooth muscle cells (e.g. postangioplasty and postatherectomy restenosis).

SO Sequence 622 AA:

Query Match 20.5%; Score 364.5; DB 21; Length 622;  
Best Local Similarity 30.4%; Pred. No. 9, 4e-19;  
Matches 88; Conservative 43; Mismatches 115; Indels 43; Gaps 8;

OY 20 RPP--PEAPQWRTRMSHGMPAGHCAAVVEG-----DPPPLTW 61  
DB 22 rpsptlpegagpw-----gapvevesflvhpqdlqlrcrlldvgslnw 66  
OY 62 TKDGRTHSGMSRFRVLPQGLKQYEREDAGYVCKATNGFSLSVNTLVLDISP 121  
DB 67 lrdgvglaes-ntrltgveevqdvpadsglyacvtspgs-dtyfsvnsdalps 124  
OY 122 KESLGPDSSSGQOE--DPASQOMARPRFTQPSKMRRYIARVGSVRLKCYASGHPR 178  
DB 125 seddddddssseketdntkpnvapywtspekmecklnavpaaktvfkcpssgtpp 184  
OY 179 DITWMDQDLTRPE----AAERKKKWTLSLKNLRPESGKTCRVSNRAGAINATYK 234  
DB 185 tlrlwknqkef-kpdmrlggykvryatwslnmsvpsdkgntclvenegslnhtyql 243  
OY 235 DVIQRTSRKSPVLGTRPVNTTDFEGGTSPOCKRSDVPRVLMKRV 283  
DB 244 dversphrpilqaglpanktvalgsnvelmckvysdppqhikwie 292

RESULT 22

AA47233  
ID AA47233 standard; Protein; 820 AA.

AC AA47233;

DT 07-SEP-1994 (first entry)

XX Human fibroblast growth factor receptor.

KW Cytomegalovirus; CMV; Towne; gH gene; escort protein;  
KW recombinant protein production; viral glycoprotein H; FGF receptor;  
KW fibroblast growth factor receptor; soluble; flg5 cDNA clone.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide

1..21  
/label= signal\_peptide

FT Protein

22..820  
/label= human\_FGF\_receptor

FT Domain

55..101  
/label= immunoglobulin-like\_domain\_1

FT /note= "extracellular"

FT Domain 176..228  
FT /label= immunoglobulin-like\_domain\_2  
FT /note= "extracellular"  
FT Domain 275..339  
FT /label= immunoglobulin-like\_domain\_3  
FT /note= "extracellular"  
FT Region 126..133  
FT /label= ARR  
FT /note= "acidic amino acid-rich region"  
FT Domain 374..395  
FT /label= transmembrane\_domain  
FT Domain 478..578  
FT /label= TK  
FT /note= "first part of split intracellular tyrosine kinase domain"  
FT Domain 593..754  
FT /label= TK  
FT /note= "second part of split intracellular tyrosine kinase domain"

PN MO9403620-A.

PD 17-FEB-1994.

PF 29-JUL-1993; 93WO-US07299.

PR 29-JUL-1992; 92US-0921807.

PA (CHIR) CHIRON CORP.

PI Spaete RL;

DR WPI; 1994-065708/08.

PT Increased expression and secretion of viral protein e.g. from  
PT cytomegalovirus from host cells - by co-expression with DNA  
PT encoding an escort protein, e.g. fibroblast growth factor  
PT receptor

PS Claim 8; Fig 6; 86pp; English.

XX Expression of recombinant viral glycoproteins on host cell surfaces  
XX can be significantly enhanced by coexpression with an escort  
XX protein. The CMV glycoprotein H polypeptide (see AA47232) is a  
XX preferred viral glycoprotein and is pref. coexpressed with human  
XX fibroblast growth factor receptor. A full-length FGF receptor cDNA,  
XX designated flg5, was isolated from a lambda ZAP human hepatoma  
XX Hep2 cDNA library; flg5 codes for a 820 amino acid protein having  
XX the sequence AA47233.

SO Sequence 820 AA:

Query Match 20.5%; Score 364.5; DB 15; Length 820;  
Best Local Similarity 30.4%; Pred. No. 1, 3e-18;  
Matches 88; Conservative 43; Mismatches 115; Indels 43; Gaps 8;

OY 20 RPP--PEAPQWRTRMSHGMPAGHCAAVVEG-----DPPPLTW 61

DB 22 rpsptlpegagpw-----gapvevesflvhpqdlqlrcrlldvgslnw 66

OY 62 TKDGRTHSGMSRFRVLPQGLKQYEREDAGYVCKATNGFSLSVNTLVLDISP 121

DB 67 lrdgvglaes-ntrltgveevqdvpadsglyacvtspgs-dtyfsvnsdalps 124

OY 122 KESLGPDSSSGQOE--DPASQOMARPRFTQPSKMRRYIARVGSVRLKCYASGHPR 178

DB 125 seddddddssseketdntkpnvapywtspekmecklnavpaaktvfkcpssgtpp 184

OY 179 DITWMDQDLTRPE----AAERKKKWTLSLKNLRPESGKTCRVSNRAGAINATYK 234

DB 185 tlrlwknqkef-kpdmrlggykvryatwslnmsvpsdkgntclvenegslnhtyql 243







## ALIGNMENTS

## RESULT 1

US-09-383-586-33  
Sequence 33, Application US/09383586  
Patent No. 6242419

## GENERAL INFORMATION:

APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Abernethy, Nevlin  
APPLICANT: Onrust, Rene  
APPLICANT: Kumble, Anand  
APPLICANT: Murison, Greg

TITLE OF INVENTION: Compounds isolated from stromal cells  
TITLE OF INVENTION: and methods for their use  
FILE REFERENCE: 11000.1037c1

CURRENT APPLICATION NUMBER: US/09/383,586  
CURRENT FILING DATE: 1999-08-26  
NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 33

LENGTH: 322

TYPE: PRT

ORGANISM: Human

US-09-383-586-33

Query Match 100.0%; Score 1779; DB 4; Length 322;  
Best Local Similarity 100.0%; Pred. No. 1.5e-150;  
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRAPECCSCCRRCGMBSPRRPPRRPQRRTRMSGRNPAHCAANVPEBPPPLTM 60  
DB 1 RRAPECCSCCRRCGMBSPRRPPRRPQRRTRMSGRNPAHCAANVPEBPPPLTM 60  
QY 61 WTKDGRTHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGSGSVNTVTLVLDISP 120  
DB 61 WTKDGRTHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGSGSVNTVTLVLDISP 120  
QY 121 GKESLGPDSGGQEDPASQOMARPRFTQPSKRRRVIAAPVGSVRLKCVASGHRPDI 180  
DB 121 GKESLGPDSGGQEDPASQOMARPRFTQPSKRRRVIAAPVGSVRLKCVASGHRPDI 180  
QY 181 TWMKDDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKVDYQRT 240  
DB 181 TWMKDDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKVDYQRT 240  
QY 241 RSKPVLGTGHPVNTVDFGGTSPQCKVRSADVYPVQMLKRVYGAEGHNSITIDVGOK 300  
DB 241 RSKPVLGTGHPVNTVDFGGTSPQCKVRSADVYPVQMLKRVYGAEGHNSITIDVGOK 300  
QY 301 FVVLPTGDVMSRPDGSYLKPL 322  
DB 301 FVVLPTGDVMSRPDGSYLKPL 322

## RESULT 2

US-09-383-586-31

Sequence 31, Application US/09383586  
Patent No. 6242419

## GENERAL INFORMATION:

APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Abernethy, Nevlin  
APPLICANT: Onrust, Rene  
APPLICANT: Kumble, Anand  
APPLICANT: Murison, Greg

TITLE OF INVENTION: Compounds isolated from stromal cells  
TITLE OF INVENTION: and methods for their use  
FILE REFERENCE: 11000.1037c1

CURRENT APPLICATION NUMBER: US/09/383,586

CURRENT FILING DATE: 1999-08-26

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31

LENGTH: 529

TYPE: PRT

ORGANISM: Mouse

US-09-383-586-31

Query Match 77.1%; Score 1371; DB 4; Length 529;  
Best Local Similarity 93.4%; Pred. No. 5.6e-114;  
Matches 255; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 50 PVEGDPPPLTMWTKDGRTHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGSGSVN 109  
DB 48 PVEGDPPPLTMWTKDGRTHSGMSRFRVLPQGLKVKQVEREDAGVYCKATNGSGSVN 107  
QY 110 YTLVYVLDISPGRKESLGPDSGGQEDPASQOMARPRFTQPSKRRRVIAAPVGSVRLK 169  
DB 108 YTLVYVLDISPGRKESLGPDSGGQEDPASQOMARPRFTQPSKRRRVIAAPVGSVRLK 167  
QY 170 CVASGHRPRDITWMDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAIN 229  
DB 168 CVASGHRPRDITWMDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAIN 227  
QY 230 ATYKVDYQRTSKRPVLTGHPVNTVDFGGTSPQCKVRSADVYPVQMLKRVYGAEGH 289  
DB 228 ATYKVDYQRTSKRPVLTGHPVNTVDFGGTSPQCKVRSADVYPVQMLKRVYGAEGH 287  
QY 290 HNSTIDVGOKFVVLPTGDVMSRPDGSYLKPL 322  
DB 288 HNSTIDVGOKFVVLPTGDVMSRPDGSYLKPL 320

## RESULT 3

US-09-383-586-32

Sequence 32, Application US/09383586  
Patent No. 6242419

## GENERAL INFORMATION:

APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Abernethy, Nevlin  
APPLICANT: Onrust, Rene  
APPLICANT: Kumble, Anand

APPLICANT: Murison, Greg  
TITLE OF INVENTION: Compounds isolated from stromal cells  
TITLE OF INVENTION: and methods for their use  
FILE REFERENCE: 11000.1037c1

CURRENT APPLICATION NUMBER: US/09/383,586  
CURRENT FILING DATE: 1999-08-26  
NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 32

LENGTH: 439

TYPE: PRT

ORGANISM: Mouse

US-09-383-586-32

Query Match 57.8%; Score 1029; DB 4; Length 439;  
Best Local Similarity 93.7%; Pred. No. 1.1e-83;  
Matches 194; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 116 DISPGKESLGPDSGGQEDPASQOMARPRFTQPSKRRRVIAAPVGSVRLKCVASGH 175  
DB 23 DISPGKESLGPDSGGQEDPASQOMARPRFTQPSKRRRVIAAPVGSVRLKCVASGH 82  
QY 176 PRPDITWMDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKYD 235  
DB 83 PRPDITWMDQALTRPEAAEPKRRKWTLSLKNLRPDSGKYTCRVSNRAGAINATYKYD 142

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